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OM protein - protein search, using sw model

Run on: July 26, 2005, 15:58:52 ; Search time 30.7159 seconds
(without alignments)

1011.008 Million cell updates/sec

Title: US-10-706-691-16

Perfect score: 2122

Sequence: 1 MKRREGALSRSALRLAPF.....TAGVHIHQEQDAGPVEISA 416

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	282	13.3	450	4	US-09-905-125A-320
3	282	13.3	450	4	US-09-902-775A-320
4	282	13.3	450	4	US-09-906-700-320
5	282	13.3	450	4	US-09-903-603A-320
6	282	13.3	450	4	US-09-904-920A-320
7	282	13.3	450	4	US-09-909-064-320
8	282	13.3	450	4	US-09-905-381A-320
9	282	13.3	450	4	US-09-906-618-320
10	281	13.2	58	4	US-09-513-999C-5729
11	220	10.4	351	3	US-08-466-465-6
12	220	10.4	351	4	US-08-730-465-6
13	202	9.5	316	4	US-09-397-243D-13
14	199.5	9.4	1101	3	US-08-986-485-2
15	197.5	9.3	365	3	US-08-928-383B-26
16	196.5	9.3	319	1	US-08-597-495B-22
17	196.5	9.3	319	3	US-08-068-051A-22
18	196.5	9.3	319	4	US-08-336-536-67
19	196.5	9.3	319	4	US-08-254-465A-6
20	196.5	9.3	319	4	US-09-953-499-6
21	196.5	9.3	387	3	US-09-175-928-2
22	193	9.1	328	4	US-09-949-016-6428
23	193	9.1	329	4	US-09-149-476-483
24	193	9.1	332	4	US-09-949-016-7327
25	191.5	9.0	365	3	US-08-928-383B-23
26	191.5	9.0	365	3	US-08-928-383B-24
27	190	9.0	383	4	US-09-949-016-11050

Sequence 5, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 6064, Ap
Sequence 4, Appli
Sequence 24, Appli
Sequence 24, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 6, Appli
Sequence 24, Appli
Sequence 4, Appli
Sequence 24, Appli
Sequence 24, Appli
Sequence 189, App
Sequence 331, App

ALIGNMENTS

RESULT 1

US-09-907-794A-320
; Sequence 320, Application US/09907794A

; Patent No. 6635468

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/907,794A

; PRIOR FILING DATE: 2001-07-17

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 320
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-794A-320

Query Match 13.3%; Score 282; DB 4; Length 450;
Best Local Similarity 31.7%; Pred. No. 1.2e-14;
Matches 72; Conservative 43; Mismatches 102; Indels 10; Gaps 7;

QY 17 LAPFVYLLLIQTDPLEGVNITSPVRLIHGTGVSALLSVQYS--STSSDRPVVKWLKR- 73
DB 3 LKVTFTLSFATGACSLKVTVPVSHTVHGVGQALYLPVHYGHTPASDIQII-WLFRP 61

QY 74 -DKPVTVVQSIGTEVIGTLRPDYDRIRLF-ENGSLLSLDIQLADEGTYEVEISIT-DDT 130
DB 62 HTMPKYLGSVNVKSVVDDL--EYQHKFTMPPNASLLINPLQFPDEGNYIVKVNIOGNGT 119

QY 131 FTGEKTNILTVDPVIRPQVLV-ASTTVLELSEAFNLCSHENGTKPSYTWLKDGPPLN 189
DB 120 LSASQKIQTVDVDPVTKVQVHPPSGAVYVGNMTLTCHVEGTRLAYQWLKNGRPVHT 179

QY 190 DSRMLLSPDQKVLITRVLMEDDDLSCMVENPISQGRSLPVKITVY 236
DB 180 SSTYSFSPQNTLHIAPTVKEDIGNYSCLVRNPVSEMSDIIMPIIY 226

RESULT 2
US-09-905-125A-320
; Sequence 320, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 320
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-125A-320

Query Match 13.3%; Score 282; DB 4; Length 450;
Best Local Similarity 31.7%; Pred. No. 1.2e-14;
Matches 72; Conservative 43; Mismatches 102; Indels 10; Gaps 7;

QY 17 LAPFVYLLLIQTDPLEGVNITSPVRLIHGTGVSALLSVQYS--STSSDRPVVKWLKR- 73
DB 3 LKVTFTLSFATGACSLKVTVPVSHTVHGVGQALYLPVHYGHTPASDIQII-WLFRP 61

QY 74 -DKPVTVVQSIGTEVIGTLRPDYDRIRLF-ENGSLLSLDIQLADEGTYEVEISIT-DDT 130
DB 62 HTMPKYLGSVNVKSVVDDL--EYQHKFTMPPNASLLINPLQFPDEGNYIVKVNIOGNGT 119

QY 131 FTGEKTNILTVDPVIRPQVLV-ASTTVLELSEAFNLCSHENGTKPSYTWLKDGPPLN 189
DB 120 LSASQKIQTVDVDPVTKVQVHPPSGAVYVGNMTLTCHVEGTRLAYQWLKNGRPVHT 179

QY 190 DSRMLLSPDQKVLITRVLMEDDDLSCMVENPISQGRSLPVKITVY 236
DB 180 SSTYSFSPQNTLHIAPTVKEDIGNYSCLVRNPVSEMSDIIMPIIY 226

RESULT 3
US-09-902-775A-320

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; Sequence 320, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 320
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-902-775A-320
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Query Match 13.3%; Score 282; DB 4; Length 450;
Best Local Similarity 31.7%; Pred. No. 1.2e-14;
Matches 72; Conservative 43; Mismatches 102; Indels 10; Gaps 7;

Qy 17 LAPEVYLLLIQTDPLEGVNITSPVRLIHGTGKSAALLSVQYS--STSSDRPVVVKQLKR- 73
Db 3 LKVFTEFLSPATGACSGLKVTVPSTHVGVGRQALYLPVHYGFHTPASDIQII-WLPERP 61
Qy 74 -DKPVTVVQSIGTEVIGTLRPDYDRIRLP-ENGSIILLSDIQLADEGTVEISIT-DDT 130
Db 62 HTMPKYLGLSVNKSVPDL--EYQHKFTMPPPNASLLINPLQFPDEGNYIVKVNIOQNGT 119
Qy 131 FTGKNTLNTVDVPISRPOVLV-ASTTVLSELAFTLNCSENGCTKPSYTWLKDQKPLLN 189
Db 120 LSASQKIQVTVDVTPVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHT 179
Qy 190 DSRMLSPDQKVLFTITRLMEDDDLYSCMVENPISQGRSLPVKITVY 236
Db 180 SSTYSFSPQNNTLHIAPTVKEDIGNYSCLVRNPVSEMSDIIMPIIY 226
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RESULT 4

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US-09-906-700-320
; Sequence 320, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,700
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
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; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 320
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-700-320

Query Match 13.3%; Score 282; DB 4; Length 450;
Best Local Similarity 31.7%; Pred. No. 1.2e-14;
Matches 72; Conservative 43; Mismatches 102; Indels 10; Gaps 7;

Qy 17 LAPFVYLLLIQTDPLEGVNITSPVRLIHGTGKSALLSVQYS--STSSDRPVVKWLKR- 73
Db 3 LKVFTTFLSFATGACSLGKVTVPSTHTVHGVRGQALYLPVHYGFTPTASDIQII-WLPERP 61

Qy 74 -DKPVTVVQSIGTEVIGTLRPDYDRIRLF-ENGSLLLSDIQLADEGTYEVEISIT-DDT 130
Db 62 HTMPKYLGSVNKSVVPDL--EYQHKFTMPPPNASLLINLPQFPDEGNYIVKVNIOGNGT 119

Qy 131 FTGEKTNLTVDVPISRPQVLV-ASTTVLESEAFNLCSHENGTKPSYTWLKDQKPLLN 189
Db 120 LSASQKIQTVDVDPVKPVQIHPFSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHT 179

Qy 190 DSRMLSPDQKVLITITRVLMDDDLLYSCMVNPISQGRSLPVKITVY 236
Db 180 SSTYSFSPQNTLHIAPTVKEDIGNYSLVRNPVSEMSDIIMPIIY 226

RESULT 5
US-09-903-603A-320
; Sequence 320, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: ROY, Margaret Ann
; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: GNE.1618P2C12
; CURRENT APPLICATION NUMBER: US/09/903,603A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
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; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 320
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-903-603A-320

Query Match 13.3%; Score 282; DB 4; Length 450;
Best Local Similarity 31.7%; Pred. No. 1.2e-14;
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Db 3 LKVFTTFLSFATGACSLGKVTVPSTHTVHGVRGQALYLPVHYGFTPTASDIQII-WLPERP 61

Qy 74 -DKPVTVVQSIGTEVIGTLRPDYDRIRLF-ENGSLLLSDIQLADEGTYEVEISIT-DDT 130
Db 62 HTMPKYLGSVNKSVVPDL--EYQHKFTMPPPNASLLINLPQFPDEGNYIVKVNIOGNGT 119

Qy 131 FTGEKTNLTVDVPISRPQVLV-ASTTVLESEAFNLCSHENGTKPSYTWLKDQKPLLN 189
Db 120 LSASQKIQTVDVDPVKPVQIHPFSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHT 179

Qy 190 DSRMLSPDQKVLITITRVLMDDDLLYSCMVNPISQGRSLPVKITVY 236
Db 180 SSTYSFSPQNTLHIAPTVKEDIGNYSLVRNPVSEMSDIIMPIIY 226

RESULT 6
US-09-904-920A-320
; Sequence 320, Application US/09904920A

```

; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,920A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 320
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-904-920A-320

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Query Match      13.3%  Score 282;  DB 4;  Length 450;
Best Local Similarity 31.7%  Pred. No. 1.2e-14;
Matches 72;  Conservative 43;  Mismatches 102;  Indels 10;  Gaps 7

Qy 17 LAPVYVLLLTCTDPLEGVNITSPVRLIHGTGKSAHSVQYS--STSSDRPVPVKWLKR- 73
Db 3 LKVFTEFLSPATGACSLKVTVPFSHTVHGVRGQALYLPVHYGFTTPASDIQII-WLFRP 61

Qy 74 -DKPVTVVQSIGTEVIGTLRPDVRDRIRLF-ENGSLLLSLDQLADEGTYEVEISIT-DDT 130
Db 62 HTMPKYLGLSNKSVVFDL--EYQHKFTMPNPASLLINLPQFPDEGNYIVKVNIGNGT 119

Qy 131 FTGKTNLTVDVPISRPQVLV-ASTTVLSEAFITLNCSHENGTKPSYTWLKGKPKLLN 189
Db 120 LSASQKIQTVTDVDPKVPVQIHPSPGAVEYVGNMNTLTCHVEGTRLAYQWLKNGRPVHT 179

Qy 190 DSRMLSPDQKVLITITVLMEDDDLVSCMVENPISQGRSLPVKITVY 236
Db 180 SSTYSFSPQNTLHIAPVTKEDIGNVSLVRNPVSEMSDIIMPIIY 226

RESULT 7
US-09-909-064-320
; Sequence 320, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,064
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089

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; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 320
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-909-064-320

Query Match 13.3%; Score 282; DB 4; Length 450;
Best Local Similarity 31.7%; Pred. No. 1.2e-14;
Matches 72; Conservative 43; Mismatches 102; Indels 10; Gaps 7;

Qy 17 LAPFVYLLLIQTDPLEGVNITSPVRLIHGTGKSALLSVQYS--STSSDRPVVKWLKR- 73
Db 3 LKVFTEFLSPATGACSGKLVTPSHTVHVGQALYLPVHYGHTPASDIQII-WLPERP 61

Qy 74 -DKPVTVVQSIGTEVIGTLRPDYDRIRLP-ENGSLLLSDLOLADEGTYEVEISIT-DDT 130
Db 62 HTMPKYLGSVKNKSVVDDL--EYQHKFTMPPNASLLINPLQFPDEGNYIVKVNIOGNGT 119

Qy 131 FTGKKTINLTVDVPISRPQVLV-ASTTVLELSEAFNLCSHENGTKPSYTWLKDGPPLN 189
Db 120 LSASQKIQVTVDVDPVTKPVVQIHPPSGAVEVGNWTLTCHVEGTRLAYQWLKNGRPVHT 179

Qy 190 DSRMLSPDQKVLITITRVLMEDDDLVSCMVENPISQGRSLPVKITVY 236
Db 180 SSTYSFSPQNTLHIAPTVKEDIGNYSCLVRNPVSEMSDIIMPIY 226

RESULT 8
US-09-905-381A-320
; Sequence 320, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,381A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 320
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-905-381A-320

Query Match 13.3%; Score 282; DB 4; Length 450;
Best Local Similarity 31.7%; Pred. No. 1.2e-14;
Matches 72; Conservative 43; Mismatches 102; Indels 10; Gaps 7;

Qy 17 LAPFVYLLLIQTDPLEGVNITSPVRLIHGTGKSALLSVQYS--STSSDRPVVKWLKR- 73
Db 3 LKVFTEFLSPATGACSGKLVTPSHTVHVGQALYLPVHYGHTPASDIQII-WLPERP 61

Qy 74 -DKPVTVVQSIGTEVIGTLRPDYDRIRLP-ENGSLLLSDLOLADEGTYEVEISIT-DDT 130
Db 62 HTMPKYLGSVKNKSVVDDL--EYQHKFTMPPNASLLINPLQFPDEGNYIVKVNIOGNGT 119

Qy 131 FTGKKTINLTVDVPISRPQVLV-ASTTVLELSEAFNLCSHENGTKPSYTWLKDGPPLN 189
Db 120 LSASQKIQVTVDVDPVTKPVVQIHPPSGAVEVGNWTLTCHVEGTRLAYQWLKNGRPVHT 179

Qy 190 DSRMLSPDQKVLITITRVLMEDDDLVSCMVENPISQGRSLPVKITVY 236
Db 180 SSTYSFSPQNTLHIAPTVKEDIGNYSCLVRNPVSEMSDIIMPIY 226

RESULT 9
US-09-906-618-320
; Sequence 320, Application US/09906618
; Patent No. 6828146

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/466,465
;; FILING DATE:
;; PRIORITY DATA:
;; PRIORITY NUMBER: PCT/US92/08755
;; FILING DATE: 06-OCT-1992
;; APPLICATION DATA:
;; APPLICATION NUMBER: US 07/862,022
;; FILING DATE: 12-APR-1992
;; PRIORITY DATA:
;; PRIORITY NUMBER: US 07/770,969
;; FILING DATE: 07-OCT-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Myers, Louis (PLM)
;; REGISTRATION NUMBER: 35,965
;; REFERENCE/DOCKET NUMBER: BGP-111CP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617)227-7400
;; TELEFAX: (617)227-7400
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 351 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-466-465-6

Query Match 10.4%; Score 220; DB 3; Length 351;
Best Local Similarity 22.9%; Pred. No. 8.8e-10;
Matches 85; Conservative 60; Mismatches 164; Indels 62; Gaps 12;
Qy 17 LAPFVYLLLIQTDPLEGVNITSPVRLIHGTGKSAALLSVQYSTSDRPVVKMQLKDKP 76
Db 8 VASFLIFNVSSKGAVSKEITNALE-TWALGQDINLDIPSFQMSDDIDDIKWEKTSK- 65
Qy 77 VTVVQSIGTEVIGTLRPD-----YRDRIRLFENGSLLLSDQLADEGTYEVEISITDFT 131
Db 66 -----KKIAQFRKEKTFKEDTKYKLFKNGLTKIKHLKTDQDIYKVSIVDTKGKN 116
Qy 132 TGEKTNLTVDVPISRPOVLVASTTVLELSEAFITLNCSEHNGTKPSVTWLKDGKPLNDS 191
Db 117 VLEKIFDLKIQRVSKPKI---SWTCINT---TLTCEVNGTDPPELNLYQDGKHLKLSQ 169
Qy 192 RMLSPQKVLITTRVLMEDEDDLYSCWVENPISQGRSLPVKITVYRSSLYIILS-TGGI 250
Db 170 RVITHKWTTSLSAK-----FKTAGNKVSKSSVEPVSCPEKGLDIYLIIGICGG 220
Qy 251 FLVTLTVTCACWKPKSKKQKLEKQNSLEYMDQNDRLKPEADTLPRSGEQRKNPMAL 310
Db 221 SLLMVFALLVFIYTKRKQKRS-----RRNDELETRAH---RVATEERGRKPHQ 267
Qy 311 YILKDKDSPETEENPAPERSATE-----PGPPGYSVS-----PAVPG-----RSPGLP 354
Db 268 IPASTPONPATSOHPPPPGHRSQAPSHRPPPPGHRVQHQPKRPPAPSGTQVHQKQGP 327
Qy 355 IRSARRYPRSP 365
Db 328 LPRPRVQPKPP 338

RESULT 12
US-09-730-465-6
Sequence 6, Application US/09730465
Patent No. 6764681
GENERAL INFORMATION:
APPLICANT: Wallner, Barbara P.
TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen
Presenting Cell Driven Skin Conditions Using
Inhibitors of the CD2/LFA-3 Interaction
NUMBER OF SEQUENCES: 8

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: LAHIVE & COCKFIELD
;; STREET: 60 State Street, Suite 510
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02109-1875
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/730,465
;; FILING DATE: 05-Dec-2000
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/08755
;; FILING DATE: 06-OCT-1992
;; APPLICATION NUMBER: US 07/862,022
;; FILING DATE: 12-APR-1992
;; APPLICATION NUMBER: US 07/770,969
;; FILING DATE: 07-OCT-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Myers, Louis (PLM)
;; REGISTRATION NUMBER: 35,965
;; REFERENCE/DOCKET NUMBER: BGP-111CP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617)227-7400
;; TELEFAX: (617)227-7400
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 351 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-730-465-6

Query Match 10.4%; Score 220; DB 4; Length 351;
Best Local Similarity 22.9%; Pred. No. 8.8e-10;
Matches 85; Conservative 60; Mismatches 164; Indels 62; Gaps 12;
Qy 17 LAPFVYLLLIQTDPLEGVNITSPVRLIHGTGKSAALLSVQYSTSDRPVVKMQLKDKP 76
Db 8 VASFLIFNVSSKGAVSKEITNALE-TWALGQDINLDIPSFQMSDDIDDIKWEKTSK- 65
Qy 77 VTVVQSIGTEVIGTLRPD-----YRDRIRLFENGSLLLSDQLADEGTYEVEISITDFT 131
Db 66 -----KKIAQFRKEKTFKEDTKYKLFKNGLTKIKHLKTDQDIYKVSIVDTKGKN 116
Qy 132 TGEKTNLTVDVPISRPOVLVASTTVLELSEAFITLNCSEHNGTKPSVTWLKDGKPLNDS 191
Db 117 VLEKIFDLKIQRVSKPKI---SWTCINT---TLTCEVNGTDPPELNLYQDGKHLKLSQ 169
Qy 192 RMLSPQKVLITTRVLMEDEDDLYSCWVENPISQGRSLPVKITVYRSSLYIILS-TGGI 250
Db 170 RVITHKWTTSLSAK-----FKTAGNKVSKSSVEPVSCPEKGLDIYLIIGICGG 220
Qy 251 FLVTLTVTCACWKPKSKKQKLEKQNSLEYMDQNDRLKPEADTLPRSGEQRKNPMAL 310
Db 221 SLLMVFALLVFIYTKRKQKRS-----RRNDELETRAH---RVATEERGRKPHQ 267
Qy 311 YILKDKDSPETEENPAPERSATE-----PGPPGYSVS-----PAVPG-----RSPGLP 354
Db 268 IPASTPONPATSOHPPPPGHRSQAPSHRPPPPGHRVQHQPKRPPAPSGTQVHQKQGP 327
Qy 355 IRSARRYPRSP 365
Db 328 LPRPRVQPKPP 338

RESULT 13
US-09-397-243D-13

```
; Sequence 13, Application US/09397243D
; Patent No. 6699688
; GENERAL INFORMATION:
; APPLICANT: Kornecki, Elizabeth
; APPLICANT: Sobocka, Malgorzata B.
; TITLE OF INVENTION: Human Platelet F11 Receptor
; FILE REFERENCE: 011.00221
; CURRENT APPLICATION NUMBER: US/09/397,243D
; CURRENT FILING DATE: 1999-09-16
; PRIOR APPLICATION NUMBER: 60/100,638
; PRIOR FILING DATE: 1998-09-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 13
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-243D-13

Query Match          9.5%; Score 202; DB 4; Length 316;
Best Local Similarity 22.7%; Pred. No. 2.2e-08;
Matches 77; Conservative 66; Mismatches 148; Indels 48; Gaps 17;

Qy 16 RLAPPVILLIQTDPLEGWITSPVRLIHGTGKSALLSVQY-SSTSSDRPVVWQKRD 74
Db 4 KMPVLTLCARVTVDAISVETPDVLRASQGSVTLPTCTYHTSTSSREGLIQDKTHT 63
Qy 75 KPVTVQSIGTEVI-GTLRPYDRIRLPEN-----GSLLSLDIQLADEGTYVEISITD 128
Db 64 ERVWIPFSNKYIHGEL---YKRVISISNAEQSDASITTDQTMADNGTYECSVLSMS 120
Qy 129 DTFTEKTI-INLTVDVPIRSQVLAFTVLESEAFVLC-SHENGTKPSYTWLKDGP 186
Db 121 DLEGTAKSRVLLVLPSPKCEGIEGTI--IGNIQLTQSKEGSTPOYSKRYN-- 176
Qy 187 LLNDSRMLLSP-DQKVLITITVLMEDDDLVSCWVENPISQGRSLPVKITVYRRS-----S 240
Db 177 ILNQEQPLAQPASQGPVSLKNIISTDTSGYICTSSN--EEGTQF-CNITVAVRSPSMVA 233
Qy 241 LYIILSTGGI--FLVLTIVTVCACWKPSKQKLEKQNSLEYMDQNDRLKPADTLPR 298
Db 234 LYVGIVGVVAALIIIGIIICCCCR-----GKDDNTE--DKEDAR--PNREAYEE 280
Qy 299 SGEQERKNPMALYILKDKDSPETENPAPEPRSPATEPGP 337
Db 281 PPEQURE-----LSREREEDDYRQEEQRSTGRESP 311

RESULT 14
US-08-986-485-2
; Sequence 2, Application US/08986485
; Patent No. 6046030
; GENERAL INFORMATION:
; APPLICANT: WU, SHUJIAN
; APPLICANT: SWEET, RAYMOND
; APPLICANT: TRUNEH, ALEMSGED
; TITLE OF INVENTION: A HUMAN LIG-1 HOMOLOG (HLIG-1)
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORCE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/986,485
; FILING DATE: 08-DEC-1997
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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/059,448
; FILING DATE: 22-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1101 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-986-485-2

Query Match          9.4%; Score 199.5; DB 3; Length 1101;
Best Local Similarity 21.3%; Pred. No. 2.1e-07;
Matches 84; Conservative 58; Mismatches 160; Indels 93; Gaps 13;

Qy 46 TVGKSALLSVQYSTSSDRPVVWQKLRDKPVTVVQSIGTEVIGTLRPDYDRIRLP--- 102
Db 617 TIRTTTVARLECAATHGNPQIAWQ---KDG-----GTDFPAKER-RMHVMP 660
Qy 103 ENGSLLSLDLQLADEGTYVEISITDFTGKEKTNLTVDVPIRSQVLAFTVLESE 162
Db 661 DDDVFFITDKIDDAGVY---SCTAQSAGSISANATLVLETSPVLPLEDVVSVGE 716
Qy 163 APTLNCSEHNGTSPSYTWLKDGPFLNDSRMLSPDOKVLTITVLMEDDDLVSCWVENP 222
Db 717 TVALQCKATGNPPPRITFWFGDRPLSLTERHLLTPDQLLVQVQVVAEDAGRYTCESNT 776
Qy 223 ISQGRSLPVKITVYRRSSVLIILSTG-----GIF-----LLVTLVTVCAWKPS 266
Db 777 LGTERA-----HSQSLVLPAGCRKDGTTVGIFTIAVSSIVLTSLVWVCIITQR 827
Qy 267 KRQKQKLEKQNSLEYMDQNDRLKPEADTLPRSGEQERKNPMALYILKDKDSPETE---E 323
Db 828 KKSE-----EYSVTNTDETVPDPVPSYLSQGTLSDRQETVTVRTEGGPQANGHIE 878
Qy 324 NPAPRPSATE-PPPGYSYSPVAPGRSPGI-----PIRSARR----- 360
Db 879 SNGVCPRDASHFPEDTHSVACRQPKLCAGSYHKPEWKAMEKAEGTFPGHKMEHGRV 938
Qy 361 -----YRSPARSPATGRTHSSPPRAPSSP 385
Db 939 CSDCNTVEVCYSRQAFHPQFVSRDQAQAPNGP 973

RESULT 15
US-08-928-383B-26
; Sequence 26, Application US/08928383B
; Patent No. 6210921
; GENERAL INFORMATION:
; APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
; APPLICANT: and Marshall S. Horwitz
; TITLE OF INVENTION: CAR, A No. 6210921el Cxsackievirus and Adenovirus
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,383B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,100
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-928-383B-26

Query Match          9.3%; Score 197.5; DB 3; Length 365;
Best Local Similarity 23.5%; Pred. No. 6.2e-08;
Matches 91; Conservative 66; Mismatches 146; Indels 85; Gaps 17;

Qy 16 RLAPFVLLLTQTDPLEGVNITSPVRLIHGTGVSALLSVQYSSTSSDR-PV-VKWLKR 73
Db 3 RLLCFVLLCGI-ADFTSGLSITTPQRIEKAKGETAVLPCKFTLSPEDQGPLDIWLI 61
Qy 74 DKPVTVVQSI-----GTEVIGTLRDYDRIRLFEN-----GSLLLSDQLAD 123
Db 62 SDNQIVDQVILYSGDKIYDNYPDILKGRVHFTSNDVKSGDASINVTNLQLSDIG 121
Qy 124 ISITDDFTTGKTLNLTVDVPISRPQVLVASTTTLVLELSEFTLNCSENGTKP-SY 182
Db 122 VKKAPG--VANKFLLTVLVKPSGTRCFVDGSE--EIGNDFKLKCEPKESLPLO 177
Qy 183 DGKPLNDSRMLLSP-----DQKVLITITRVLMEDDLSCMVENPISQGRSLPVK 237
Db 178 -----LSDSQTMPTPLAEMTSPVISVKNASSEYSGTYSCTVQNRVGSQDCM-L 231
Qy 238 RSSLYIILSTGGIFLLVTLTVCA-----CWKPSKXKQKKLEKQNSLEYMDQ 293
Db 232 PSNRAGTIAGAVIGTLALVLIGAILFCCHR--KRREEKYEKE-----VHHD 278
Qy 294 DTLPRSGQERKNPMALYILKDKDSPETEENPAPEPRSATPEP---GPPGYSV 350
Db 279 -----EDVPPPKSRTSTARSYIGNSHSLGMSPSNM 310
Qy 351 PG-----LPISRARYPRSPARSPA 370
Db 311 EGYSKTQYNQVPSEDFERAPQSTLAPA 338
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Search completed: July 26, 2005, 16:15:52
Job time : 31.7159 secs

Qy 61 SSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRDPYDRIRLRFENGSLLLSDQLADEGTY 120
Db 61 SSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRDPYDRIRLRFENGSLLLSDQLADEGTY 120
Qy 121 EVEISITDDTFTGKTLINLTVDVPISRPQVLVASTTVLESEAFNLCSHENGTKPSYTW 180
Db 121 EVEISITDDTFTGKTLINLTVDVPISRPQVLVASTTVLESEAFNLCSHENGTKPSYTW 180
Qy 181 LKDGKPLNDSRMLLSPDQKVLITTRVLMEDDDLYSCWENPISQGRSLPVKITVYRRSS 240
Db 181 LKDGKPLNDSRMLLSPDQKVLITTRVLMEDDDLYSCWENPISQGRSLPVKITVYRRSS 240
Qy 241 LYIILSTGGIFLLVTLVTVCAWKPSKRQKKLEKQNSLEYMDQNDRLKPEADTLPRSG 300
Db 241 LYIILSTGGIFLLVTLVTVCAWKPSKRQKKLEKQNSLEYMDQNDRLKPEADTLPRSG 300
Qy 301 EQERKNPMALYILKDKSPETEENPAPEPRSATPPGPGYSVSPVPGRSPGLPIRSARR 360
Db 301 EQERKNPMALYILKDKSPETEENPAPEPRSATPPGPGYSVSPVPGRSPGLPIRSARR 360
Qy 361 YPRSPARSPATGRTHSSPPRAPSPGRSRASRTLRTAGVHIIREQDEAGPVEISA 416
Db 361 YPRSPARSPATGRTHSSPPRAPSPGRSRASRTLRTAGVHIIREQDEAGPVEISA 416
RESULT 2
US-10-706-691-41
; Sequence 41, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10/706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 41
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-41
Query Match 100.0%; Score 2122; DB 16; Length 416;
Best Local Similarity 100.0%; Pred. No. 3.3e-138;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKRERGALSASRALRPAFFVYLLLIQTDPLEGVNITSPVRLIHGTGKSALLSVQYSST 60
Db 1 MKRERGALSASRALRPAFFVYLLLIQTDPLEGVNITSPVRLIHGTGKSALLSVQYSST 60
Qy 61 SSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRDPYDRIRLRFENGSLLLSDQLADEGTY 120
Db 61 SSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRDPYDRIRLRFENGSLLLSDQLADEGTY 120
Qy 121 EVEISITDDTFTGKTLINLTVDVPISRPQVLVASTTVLESEAFNLCSHENGTKPSYTW 180
Db 121 EVEISITDDTFTGKTLINLTVDVPISRPQVLVASTTVLESEAFNLCSHENGTKPSYTW 180
Qy 181 LKDGKPLNDSRMLLSPDQKVLITTRVLMEDDDLYSCWENPISQGRSLPVKITVYRRSS 240
Db 181 LKDGKPLNDSRMLLSPDQKVLITTRVLMEDDDLYSCWENPISQGRSLPVKITVYRRSS 240
Qy 241 LYIILSTGGIFLLVTLVTVCAWKPSKRQKKLEKQNSLEYMDQNDRLKPEADTLPRSG 300
Db 241 LYIILSTGGIFLLVTLVTVCAWKPSKRQKKLEKQNSLEYMDQNDRLKPEADTLPRSG 300
Qy 301 EQERKNPMALYILKDKSPETEENPAPEPRSATPPGPGYSVSPVPGRSPGLPIRSARR 360
Db 301 EQERKNPMALYILKDKSPETEENPAPEPRSATPPGPGYSVSPVPGRSPGLPIRSARR 360
Qy 361 YPRSPARSPATGRTHSSPPRAPSPGRSRASRTLRTAGVHIIREQDEAGPVEISA 416
Db 361 YPRSPARSPATGRTHSSPPRAPSPGRSRASRTLRTAGVHIIREQDEAGPVEISA 416

Qy 241 LYIILSTGGIFLLVTLVTVCAWKPSKRQKKLEKQNSLEYMDQNDRLKPEADTLPRSG 300
Db 241 LYIILSTGGIFLLVTLVTVCAWKPSKRQKKLEKQNSLEYMDQNDRLKPEADTLPRSG 300
Qy 301 EQERKNPMALYILKDKSPETEENPAPEPRSATPPGPGYSVSPVPGRSPGLPIRSARR 360
Db 301 EQERKNPMALYILKDKSPETEENPAPEPRSATPPGPGYSVSPVPGRSPGLPIRSARR 360
Qy 361 YPRSPARSPATGRTHSSPPRAPSPGRSRASRTLRTAGVHIIREQDEAGPVEISA 416
Db 361 YPRSPARSPATGRTHSSPPRAPSPGRSRASRTLRTAGVHIIREQDEAGPVEISA 416
RESULT 3
US-10-706-691-18
; Sequence 18, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10/706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 18
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-18
Query Match 93.9%; Score 1992; DB 16; Length 418;
Best Local Similarity 94.3%; Pred. No. 3.2e-129;
Matches 394; Conservative 10; Mismatches 12; Indels 2; Gaps 1;
Qy 1 MKRERGALSASRALRPAFFVYLLLIQTDPLEGVNITSPVRLIHGTGKSALLSVQYSST 60
Db 1 MKRERGALSASRALRPAFFVYLLLIQTDPLEGVNITSPVRLIHGTGKSALLSVQYSST 60
Qy 61 SSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRDPYDRIRLRFENGSLLLSDQLADEGTY 120
Db 61 SSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRDPYDRIRLRFENGSLLLSDQLADEGTY 120
Qy 121 EVEISITDDTFTGKTLINLTVDVPISRPQVLVASTTVLESEAFNLCSHENGTKPSYTW 180
Db 121 EVEISITDDTFTGKTLINLTVDVPISRPQVLVASTTVLESEAFNLCSHENGTKPSYTW 180
Qy 181 LKDGKPLNDSRMLLSPDQKVLITTRVLMEDDDLYSCWENPISQGRSLPVKITVYRRSS 240
Db 181 LKDGKPLNDSRMLLSPDQKVLITTRVLMEDDDLYSCWENPISQGRSLPVKITVYRRSS 240
Qy 241 LYIILSTGGIFLLVTLVTVCAWKPSKRQKKLEKQNSLEYMDQNDRLKPEADTLPR 298
Db 241 LYIILSTGGIFLLVTLVTVCAWKPSKRQKKLEKQNSLEYMDQNDRLKPEADTLPR 300
Qy 299 SGOERKNPMALYILKDKSPETEENPAPEPRSATPPGPGYSVSPVPGRSPGLPIRSA 358
Db 301 SGOERKNPMALYILKDKSPEDENPATPRSTTEPGPGYSVSPVPGRSPGLPIRSA 360
Qy 359 RYPRSPARSPATGRTHSSPPRAPSPGRSRASRTLRTAGVHIIREQDEAGPVEISA 416
Db 361 RYPRSPARSPATGRTHSSPPRAPSPGRSRASRTLRTAGVHIIREQDEAGPVEISA 418

RESULT 4

US-10-706-691-26
; Sequence 26, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boechert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10/706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 26
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-26

Query Match 92.5%; Score 1962; DB 16; Length 383;
Best Local Similarity 100.0%; Pred. No. 3.3e-127; Mismatches 0; Indels 0; Gaps 0;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 VNITSPVRLIHGTGKSAALLSVQYSSSTSSDRPVVKWQKRDKPTVVQSIGTEVIGTLRP 93
Db 1 VNITSPVRLIHGTGKSAALLSVQYSSSTSSDRPVVKWQKRDKPTVVQSIGTEVIGTLRP 60

Qy 94 DYRDIRLFENGSLLSLDLADEGTVEVEISITDDTFTGKTNLTVDVPISRPQVLVA 153
Db 61 DYRDIRLFENGSLLSLDLADEGTVEVEISITDDTFTGKTNLTVDVPISRPQVLVA 120

Qy 154 STTVLELSEATLNCSEHNGTKPSYTWLKDQKPLNDSRMLLSPDQKVLITTRVLMEDDD 213
Db 121 STTVLELSEATLNCSEHNGTKPSYTWLKDQKPLNDSRMLLSPDQKVLITTRVLMEDDD 180

Qy 214 LYSQWENPISQGRSLPVKTIIVYRRSSLYIILSTGGIFLLVTVVCACWKPSKRRKOKKL 273
Db 181 LYSQWENPISQGRSLPVKTIIVYRRSSLYIILSTGGIFLLVTVVCACWKPSKRRKOKKL 240

Qy 274 EKQNSLEYMQNDRLKPEADTLPRSGEQERKNPMALYILKDKDSPETEENPAPEPRSAT 333
Db 241 EKQNSLEYMQNDRLKPEADTLPRSGEQERKNPMALYILKDKDSPETEENPAPEPRSAT 300

Qy 334 EPGPFGYSVSPAVPGSRPLGPIRSGARRYPSPARSPATGRTHSSPPRAPPSPGSRGASR 393
Db 301 EPGPFGYSVSPAVPGSRPLGPIRSGARRYPSPARSPATGRTHSSPPRAPPSPGSRGASR 360

Qy 394 TLRTAGVHIIRQDEAGPVEISA 416
Db 361 TLRTAGVHIIRQDEAGPVEISA 383

RESULT 5

US-10-432-103-4
; Sequence 4, Application US/10432103
; Publication No. US20040043424A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dying Aina M.
; APPLICANT: YUE, Henry
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: LU, Yan

; APPLICANT: LO, Terrence P.
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: ARVIZU, Chandra
; APPLICANT: YAO, Monique G.
; TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS
; FILE REFERENCE: PF-0841 PCT
; CURRENT APPLICATION NUMBER: US/10/432,103
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: 60/249,645
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040043424A1 5831801CD1
US-10-432-103-4

Query Match 69.4%; Score 1472; DB 15; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.7e-93;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKRERGALSRAALRIAPFVYLLLIOTDPLEGVNITSPVRLIHGTGKSAALLSVQYSSST 60
Db 1 MKRERGALSRAALRIAPFVYLLLIOTDPLEGVNITSPVRLIHGTGKSAALLSVQYSSST 60

Qy 61 SSDRPVVKWQKRDKPTVVQSIGTEVIGTLRPDYRDIRLFENGSLLSLDLADEGT 120
Db 61 SSDRPVVKWQKRDKPTVVQSIGTEVIGTLRPDYRDIRLFENGSLLSLDLADEGT 120

Qy 121 EVEISITDDTFTGKTNLTVDVPISRPQVLVA VASTTVLESEATLNCSEHNGTKPSYTW 180
Db 121 EVEISITDDTFTGKTNLTVDVPISRPQVLVA VASTTVLESEATLNCSEHNGTKPSYTW 180

Qy 181 LKDGKPLNDSRMLLSPDQKVLITTRVLMEDDDLYSCWENPISQGRSLPVKTIIVYRRSS 240
Db 181 LKDGKPLNDSRMLLSPDQKVLITTRVLMEDDDLYSCWENPISQGRSLPVKTIIVYRRSS 240

Qy 241 LYIILSTGGIFLLVTVVCACWKPSKRRKOKKLEKQNSLEYMQNDRLK 291
Db 241 LYIILSTGGIFLLVTVVCACWKPSKRRKOKKLEKQNSLEYMQNDRLK 291

RESULT 6

US-10-706-691-20
; Sequence 20, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boechert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10/706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 20
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-20

Query Match 56.8%; Score 1205; DB 16; Length 240;
Best Local Similarity 100.0%; Pred. No. 3.4e-75;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKRERGALSRRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTGKSGALLSVQYSST 60
Db 1 MKRERGALSRRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTGKSGALLSVQYSST 60

Qy 61 SSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRDPYRDRIRLFENGSLLLSDQLADEGTY 120
Db 61 SSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRDPYRDRIRLFENGSLLLSDQLADEGTY 120

Qy 121 EVELSIITDDFTTGKTLNLTVDVPISRPQVLVASTTVLESEAFNLCSHENGTKPSYTW 180
Db 121 EVELSIITDDFTTGKTLNLTVDVPISRPQVLVASTTVLESEAFNLCSHENGTKPSYTW 180

Qy 181 LKDGKPLNDSRMLLSPPQKVLITTRVLMEDEDDLLYSQWENPISQGRSLPVKITVYRRSS 240
Db 181 LKDGKPLNDSRMLLSPPQKVLITTRVLMEDEDDLLYSQWENPISQGRSLPVKITVYRRSS 240

RESULT 7

US-10-706-691-43
; Sequence 43, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10/706.691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 43
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-706-691-43

Query Match 56.8%; Score 1205; DB 16; Length 246;
Best Local Similarity 100.0%; Pred. No. 3.5e-75;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKRERGALSRRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTGKSGALLSVQYSST 60
Db 1 MKRERGALSRRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTGKSGALLSVQYSST 60

Qy 61 SSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRDPYRDRIRLFENGSLLLSDQLADEGTY 120
Db 61 SSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRDPYRDRIRLFENGSLLLSDQLADEGTY 120

Qy 121 EVELSIITDDFTTGKTLNLTVDVPISRPQVLVASTTVLESEAFNLCSHENGTKPSYTW 180
Db 121 EVELSIITDDFTTGKTLNLTVDVPISRPQVLVASTTVLESEAFNLCSHENGTKPSYTW 180

Qy 181 LKDGKPLNDSRMLLSPPQKVLITTRVLMEDEDDLLYSQWENPISQGRSLPVKITVYRRSS 240
Db 181 LKDGKPLNDSRMLLSPPQKVLITTRVLMEDEDDLLYSQWENPISQGRSLPVKITVYRRSS 240

RESULT 8

US-10-112-944-434
; Sequence 434, Application US/10112944

Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112.944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: pt_FL_genes Version 5.0
; SEQ ID NO 434
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-112-944-434

Query Match 56.0%; Score 1189; DB 15; Length 256;
Best Local Similarity 96.7%; Pred. No. 4.7e-74;
Matches 236; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKRERGALSRRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTGKSGALLSVQYSST 60
Db 1 MKRERGALSRRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTGKSGALLSVQYSST 60

Qy 61 SSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRDPYRDRIRLFENGSLLLSDQLADEGTY 120
Db 61 SSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRDPYRDRIRLFENGSLLLSDQLADEGTY 120

Qy 121 EVELSIITDDFTTGKTLNLTVDVPISRPQVLVASTTVLESEAFNLCSHENGTKPSYTW 180
Db 121 EVELSIITDDFTTGKTLNLTVDVPISRPQVLVASTTVLESEAFNLCSHENGTKPSYTW 180

Qy 181 LKDGKPLNDSRMLLSPPQKVLITTRVLMEDEDDLLYSQWENPISQGRSLPVKITVYRRSS 240
Db 181 LKDGKPLNDSRMLLSPPQKVLITTRVLMEDEDDLLYSQWENPISQGRSLPVKITVYRRSS 240

Qy 241 LYII 244
Db 241 FYII 244

RESULT 9

US-10-112-944-880
; Sequence 880, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:

```
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
; TITLE OF INVENTION: Secreted Polypeptides
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: pc_FL_genes Version 5.0
; SEQ ID NO 880
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: incyte ID No. US20040049010A1 382654CDI
US-10-112-944-880

Query Match 55.5%; Score 1178; DB 15; Length 256;
Best Local Similarity 97.1%; Pred. No. 2.7e-73;
Matches 234; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKRERGALSRSRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTWCKSALLSVQYSST 60
Db 1 MKRERGALSRSRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTWCKSALLSVQYSST 60
Qy 61 SSDRPVVKWQKRDKPVTWVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSLQLADEGTY 120
Db 61 SSDRPVVKWQKRDKPVTWVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSLQLADEGTY 120
Qy 121 EVEISITDDTFTGKTNLTVDVPISRQVILVASTTVLELSEAFLLNCSHENGKPSYTW 180
Db 121 EVEISITDDTFTGKTNLTVDVPISRQVILVASTTVLELSEAFLLNCSHENGKPSYTW 180
Qy 181 LKDGKPLNDRMSSLSPDKVLTITRVLMEDDDLSCMVENPISQGRSLPKVITVYRRSS 240
Db 181 LKDGKPLNDRMSSLSPDKVLTITRVLMEDDDLSCMVENPISQGRSLPKVITVYRRSS 240
Qy 241 L 241
Db 241 L 241

RESULT 10
US-10-415-188-7
; Sequence 7, Application US/10415188
; Publication No. US20040049010A1
; GENERAL INFORMATION:
; APPLICANT: WARREN, Bridget A.; XU, Yuming;
; APPLICANT: YUE, Henry; BATRA, Sajeev;

; APPLICANT: BURFORD, Neil; GANDHI, Ameena R.;
; APPLICANT: CHAWLA, Narinder K.; ARVIZU, Chandra S.;
; APPLICANT: TANG, Y. Tom; LU, Dyung Aina M.;
; APPLICANT: DUGGAN, Brendan M.; BAUGHN, Mariah R.;
; APPLICANT: LEE, Ernestine A.; KHAN, Farran A.;
; APPLICANT: NGUYEN, Damiel B.; AZIMZAI, Yalda;
; APPLICANT: YAO, Monique G.; LAL, Preeti G.;
; APPLICANT: THANGAVELU, Kavitha; RAMKUMAR, Jayalaxmi;
; APPLICANT: TRAN, Bao; DING, Li;
; APPLICANT: AU-YOUNG, Janice
; TITLE OF INVENTION: TRANSMEMBRANE PROTEINS
; FILE REFERENCE: PF-0836 USN
; CURRENT APPLICATION NUMBER: US/10/415,188
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: PCT/US01/49670
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/244,017
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/252,855
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/251,825
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/255,085
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: incyte ID No. US20040049010A1 382654CDI
US-10-415-188-7

Query Match 54.5%; Score 1157; DB 15; Length 224;
Best Local Similarity 100.0%; Pred. No. 6.5e-72;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 MLISPDQKVLITRVLMEDDDLSCMVENPISQGRSLPKVITVYRRSSLYILSTGGIFL 252
Db 1 MLISPDQKVLITRVLMEDDDLSCMVENPISQGRSLPKVITVYRRSSLYILSTGGIFL 60
Qy 253 LVTLVTWCACWKSRRQKKLEKONSLEYMDQNDRLKPEADTLPKSGEQERKNPMALYI 312
Db 61 LVTLVTWCACWKSRRQKKLEKONSLEYMDQNDRLKPEADTLPKSGEQERKNPMALYI 120
Qy 313 LKDKDSPETENPAPEPRSPATEPGPGYSPVAVPGSPGLPIRSARYPRSPARSPATG 372
Db 121 LKDKDSPETENPAPEPRSPATEPGPGYSPVAVPGSPGLPIRSARYPRSPARSPATG 180
Qy 373 RTHSSPPRAPSSPGRSRSASRTLTAGVHIIRREQDEAGPVEISA 416
Db 181 RTHSSPPRAPSSPGRSRSASRTLTAGVHIIRREQDEAGPVEISA 224

RESULT 11
US-10-706-691-22
; Sequence 22, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10/706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
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; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 22
; LENGTH: 207
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-706-691-22

Query Match      49.2%; Score 1045; DB 16; Length 207;
Best Local Similarity 100.0%; Pred. No. 3.2e-64;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 VNITSPVRLIHGTGKSAALLSVQYSSSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 93
Db 1 VNITSPVRLIHGTGKSAALLSVQYSSSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 60

Qy 94 DYDRIRLRFENGSLLLSDQLADGTYEVEISITDDTFTGKTNLTVDPISRPQVLVA 153
Db 61 DYDRIRLRFENGSLLLSDQLADGTYEVEISITDDTFTGKTNLTVDPISRPQVLVA 120

Qy 154 STTVLEISEAFTLNCSEHNGTKPSYTWLKGKPLNDSRMLLSPDKVLITRVLMBDD 213
Db 121 STTVLEISEAFTLNCSEHNGTKPSYTWLKGKPLNDSRMLLSPDKVLITRVLMBDD 180

Qy 214 LYSWCVENPISQGRSLPVKITVYRRSS 240
Db 181 LYSWCVENPISQGRSLPVKITVYRRSS 207

RESULT 12
US-10-706-691-4
; Sequence 4, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; CURRENT APPLICATION NUMBER: US/10/706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 4
; LENGTH: 114
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-706-691-4

Query Match      26.9%; Score 570; DB 16; Length 114;
Best Local Similarity 100.0%; Pred. No. 9.2e-32;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 PLEGVNITSPVRLIHGTGKSAALLSVQYSSSTSDRPVVKWQKRDKPVTVVQSIGTEVIG 89
Db 1 PLEGVNITSPVRLIHGTGKSAALLSVQYSSSTSDRPVVKWQKRDKPVTVVQSIGTEVIG 60

Qy 90 TLRPDYRIRLRFENGSLLLSDQLADGTYEVEISITDDTFTGKTNLTVDV 143
Db 61 TLRPDYRIRLRFENGSLLLSDQLADGTYEVEISITDDTFTGKTNLTVDV 114

RESULT 13
US-10-706-691-24
; Sequence 24, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10/706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 14
; LENGTH: 100
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-706-691-14

Query Match      24.6%; Score 522; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.6e-28;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 317 DSPETENPAPEPRSATPGPGYVSVPVPGSPGLPIRSARYPRSPARSPATGRTHS 376
Db 1 DSPETENPAPEPRSATPGPGYVSVPVPGSPGLPIRSARYPRSPARSPATGRTHS 60
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QY 377 SPPRAPSSGSRASRTLRITAGVHIIREQDEAGPVEISA 416
 Db 61 SPPRAPSSGSRASRTLRITAGVHIIREQDEAGPVEISA 100

RESULT 15

US-10-706-691-6
 ; Sequence 6, Application US/10706691
 ; Publication No. US20040204352A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Davids, Andrew Robert
 ; APPLICANT: Fagan, Richard Joseph
 ; APPLICANT: Phelps, Christopher Benjamin
 ; APPLICANT: Power, Christine
 ; APPLICANT: Chvatchko, Yolande
 ; APPLICANT: Boschert, Ursula
 ; TITLE OF INVENTION: Cytokine antagonist molecules
 ; FILE REFERENCE: 674582-2001
 ; CURRENT APPLICATION NUMBER: US/10/706,691
 ; CURRENT FILING DATE: 2003-11-12
 ; PRIOR APPLICATION NUMBER: PCT/GB03/01851
 ; PRIOR FILING DATE: 2003-04-30
 ; PRIOR APPLICATION NUMBER: GB 0209884.6
 ; PRIOR FILING DATE: 2002-04-30
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: SeqWin99, version 1.02
 ; SEQ ID NO 6
 ; LENGTH: 94
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-706-691-6

Query Match 22.8%; Score 484; DB 16; Length 94;
 Best Local Similarity 100.0%; Pred. No. 6.3e-26;
 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 144 PISRPQVLVASTTVLESEAFNLCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKYL 203
 Db 1 PISRPQVLVASTTVLESEAFNLCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKYL 60
 QY 204 ITRVLMEDDDLVSCWVENPISQGRSLPVKITVYR 237
 Db 61 ITRVLMEDDDLVSCWVENPISQGRSLPVKITVYR 94

Search completed: July 26, 2005, 16:21:17
 Job time : 108.504 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 16:01:42 ; Search time 61.4446 Seconds

(without alignments)
1519.387 Million cell updates/sec

Title: US-10-706-691-20

Perfect score: 1205

Sequence: 1 MKRRGALSRASRLRLAPF.....NPISGRSLPVKITVRRSS 240

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09C_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10E_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1205	100.0	240	16	US-10-706-691-20
2	1205	100.0	246	16	US-10-706-691-43
3	1205	100.0	298	15	US-10-432-103-4
4	1205	100.0	416	16	US-10-706-691-16
5	1205	100.0	416	16	US-10-706-691-41
6	1174	97.4	256	15	US-10-112-944-434
7	1174	97.4	256	15	US-10-112-944-880
8	1171	97.2	418	16	US-10-706-691-18
9	1045	86.7	207	16	US-10-706-691-22
10	1045	86.7	383	16	US-10-706-691-26
11	570	47.3	114	16	US-10-706-691-4

12	548	45.5	110	16	US-10-706-691-24	Sequence 24, App1
13	484	40.2	94	16	US-10-706-691-6	Sequence 6, App1
14	282	23.4	450	9	US-09-909-320-320	Sequence 320, App
15	282	23.4	450	9	US-09-909-088B-320	Sequence 320, App
16	282	23.4	450	9	US-09-905-281A-320	Sequence 320, App
17	282	23.4	450	9	US-09-902-853-320	Sequence 320, App
18	282	23.4	450	9	US-09-907-824-320	Sequence 320, App
19	282	23.4	450	9	US-09-907-841-320	Sequence 320, App
20	282	23.4	450	10	US-09-904-611-320	Sequence 320, App
21	282	23.4	450	10	US-09-903-640-320	Sequence 320, App
22	282	23.4	450	10	US-09-908-093-320	Sequence 320, App
23	282	23.4	450	10	US-09-906-742-320	Sequence 320, App
24	282	23.4	450	10	US-09-906-838-320	Sequence 320, App
25	282	23.4	450	10	US-09-907-613-320	Sequence 320, App
26	282	23.4	450	10	US-09-907-842-320	Sequence 320, App
27	282	23.4	450	10	US-09-904-859-320	Sequence 320, App
28	282	23.4	450	10	US-09-909-204-320	Sequence 320, App
29	282	23.4	450	10	US-09-904-820-320	Sequence 320, App
30	282	23.4	450	10	US-09-904-786-320	Sequence 320, App
31	282	23.4	450	10	US-09-906-646-320	Sequence 320, App
32	282	23.4	450	10	US-09-906-700-320	Sequence 320, App
33	282	23.4	450	10	US-09-903-786-320	Sequence 320, App
34	282	23.4	450	10	US-09-902-903-320	Sequence 320, App
35	282	23.4	450	10	US-09-903-749A-320	Sequence 320, App
36	282	23.4	450	10	US-09-904-119-320	Sequence 320, App
37	282	23.4	450	10	US-09-904-956-320	Sequence 320, App
38	282	23.4	450	10	US-09-902-736-320	Sequence 320, App
39	282	23.4	450	10	US-09-907-794-320	Sequence 320, App
40	282	23.4	450	10	US-09-903-943-320	Sequence 320, App
41	282	23.4	450	10	US-09-904-462-320	Sequence 320, App
42	282	23.4	450	10	US-09-907-925-320	Sequence 320, App
43	282	23.4	450	10	US-09-902-692-320	Sequence 320, App
44	282	23.4	450	10	US-09-903-520-320	Sequence 320, App
45	282	23.4	450	10	US-09-903-056-320	Sequence 320, App

ALIGNMENTS

RESULT 1
US-10-706-691-20
Sequence 20, Application US/10706691
Publication No. US20040204352A1
GENERAL INFORMATION:
APPLICANT: Davids, Andrew Robert
APPLICANT: Fagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Power, Christine
APPLICANT: Chvatchko, Yolande
APPLICANT: Boschart, Ursula
TITLE OF INVENTION: Cytokine antagonist molecules
FILE REFERENCE: 674582-2001
CURRENT APPLICATION NUMBER: US/10/706,691
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/GB03/01851
PRIOR FILING DATE: 2003-04-30
PRIOR APPLICATION NUMBER: GB 0209884.6
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Seqwin9, version 1.02
SEQ ID NO 20
LENGTH: 240
TYPE: PRT
ORGANISM: Homo sapiens
US-10-706-691-20
Query Match 100.0%; Score 1205; DB 16; Length 240;
Best Local Similarity 100.0%; Pred. No. 5.5e-102;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKRRGALSRASRLRLAPFYLLIOTDPLEGVNITSPPVRLHGTGKSLLSVQYSST 60
Db 1 MKRRGALSRASRLRLAPFYLLIOTDPLEGVNITSPPVRLHGTGKSLLSVQYSST 60

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QY 61 SSDRPVVMKQIKRDKPVTWVOSIGTEVIGTLRPDYRDIRLFEENGSLLSPLQADDEGTY 120
Db 61 SSDRPVVMKQIKRDKPVTWVOSIGTEVIGTLRPDYRDIRLFEENGSLLSPLQADDEGTY 120
QY 121 EVEISITDDPTGKKTINLTVDVPISRPQVLVASTTVLESEAFTLNCSHENGTKPSYTW 180
Db 121 EVEISITDDPTGKKTINLTVDVPISRPQVLVASTTVLESEAFTLNCSHENGTKPSYTW 180
QY 181 LKDGKPLNDSRMLSPDQKVLITTRVLMEDDDLSCWENPISQGRSLPVKITVYRRSS 240
Db 181 LKDGKPLNDSRMLSPDQKVLITTRVLMEDDDLSCWENPISQGRSLPVKITVYRRSS 240
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RESULT 2
US-10-706-691-43

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; Sequence 43, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10/706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 43
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-43
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Query Match 100.0%; Score 1205; DB 16; Length 246;
Best Local Similarity 100.0%; Pred. No. 5.7e-102;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MKRERGALSRSARLRLAPFYVLLLIOTDPLEGVNITSPVRLIHGTGKSALLSVQYSST 60
Db 1 MKRERGALSRSARLRLAPFYVLLLIOTDPLEGVNITSPVRLIHGTGKSALLSVQYSST 60
QY 61 SSDRPVVMKQIKRDKPVTWVOSIGTEVIGTLRPDYRDIRLFEENGSLLSPLQADDEGTY 120
Db 61 SSDRPVVMKQIKRDKPVTWVOSIGTEVIGTLRPDYRDIRLFEENGSLLSPLQADDEGTY 120
QY 121 EVEISITDDPTGKKTINLTVDVPISRPQVLVASTTVLESEAFTLNCSHENGTKPSYTW 180
Db 121 EVEISITDDPTGKKTINLTVDVPISRPQVLVASTTVLESEAFTLNCSHENGTKPSYTW 180
QY 181 LKDGKPLNDSRMLSPDQKVLITTRVLMEDDDLSCWENPISQGRSLPVKITVYRRSS 240
Db 181 LKDGKPLNDSRMLSPDQKVLITTRVLMEDDDLSCWENPISQGRSLPVKITVYRRSS 240
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RESULT 3
US-10-432-103-4

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; Sequence 4, Application US/10432103
; Publication No. US20040043424A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dying Aina M.
; APPLICANT: YUE, Henry
; APPLICANT: ELIOTT, Vicki S.
; APPLICANT: THANGAVELU, Kavitha
```

```
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: LU, Yan
; APPLICANT: LO, Terrence P.
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: GANDHI, Ameena K.
; APPLICANT: ARVIZU, Chandra
; APPLICANT: YAO, Monique G.
; TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS
; FILE REFERENCE: PF-0841 PCT
; CURRENT APPLICATION NUMBER: US/10/432,103
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: 60/249,645
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040043424A1 5831801CD1
US-10-432-103-4
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Query Match 100.0%; Score 1205; DB 15; Length 298;
Best Local Similarity 100.0%; Pred. No. 7.4e-102;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MKRERGALSRSARLRLAPFYVLLLIOTDPLEGVNITSPVRLIHGTGKSALLSVQYSST 60
Db 1 MKRERGALSRSARLRLAPFYVLLLIOTDPLEGVNITSPVRLIHGTGKSALLSVQYSST 60
QY 61 SSDRPVVMKQIKRDKPVTWVOSIGTEVIGTLRPDYRDIRLFEENGSLLSPLQADDEGTY 120
Db 61 SSDRPVVMKQIKRDKPVTWVOSIGTEVIGTLRPDYRDIRLFEENGSLLSPLQADDEGTY 120
QY 121 EVEISITDDPTGKKTINLTVDVPISRPQVLVASTTVLESEAFTLNCSHENGTKPSYTW 180
Db 121 EVEISITDDPTGKKTINLTVDVPISRPQVLVASTTVLESEAFTLNCSHENGTKPSYTW 180
QY 181 LKDGKPLNDSRMLSPDQKVLITTRVLMEDDDLSCWENPISQGRSLPVKITVYRRSS 240
Db 181 LKDGKPLNDSRMLSPDQKVLITTRVLMEDDDLSCWENPISQGRSLPVKITVYRRSS 240
```

RESULT 4
US-10-706-691-16

```
; Sequence 16, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10/706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 16
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-16
```

```
Query Match 100.0%; Score 1205; DB 16; Length 416;
```

Best Local Similarity 100.0%; Pred. No. 1.2e-101;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 MKRREGALSRSARLRLAPFYVLLLIQTDPLEGVNITSPVRLIHGTGKALLSVQYST 60
    1 MKRREGALSRSARLRLAPFYVLLLIQTDPLEGVNITSPVRLIHGTGKALLSVQYST 60
Db 1 MKRREGALSRSARLRLAPFYVLLLIQTDPLEGVNITSPVRLIHGTGKALLSVQYST 60
Qy 61 SSDRPVVMQKLRKDPVTVVOSIGTEVIGTLRPDVRDRIRLFENGSLLSLQIADDEGY 120
    61 SSDRPVVMQKLRKDPVTVVOSIGTEVIGTLRPDVRDRIRLFENGSLLSLQIADDEGY 120
Db 61 SSDRPVVMQKLRKDPVTVVOSIGTEVIGTLRPDVRDRIRLFENGSLLSLQIADDEGY 120
Qy 121 EVEISITDPTGKKTINLTVDPVISRPOVLVASTTVLESEAFLLNCSHENGTKPSYTW 180
    121 EVEISITDPTGKKTINLTVDPVISRPOVLVASTTVLESEAFLLNCSHENGTKPSYTW 180
Db 121 EVEISITDPTGKKTINLTVDPVISRPOVLVASTTVLESEAFLLNCSHENGTKPSYTW 180
Qy 181 LKDGKPLNDSRMLSPDQKVLITTRVLMEDDDLYSCWENPISQGRSLPVKITVYRRSS 240
    181 LKDGKPLNDSRMLSPDQKVLITTRVLMEDDDLYSCWENPISQGRSLPVKITVYRRSS 240
Db 181 LKDGKPLNDSRMLSPDQKVLITTRVLMEDDDLYSCWENPISQGRSLPVKITVYRRSS 240

```

RESULT 5

US-10-706-691-41

; Sequence 41, Application US/10706691
; Publication No. US20040204352A1

; GENERAL INFORMATION:

; APPLICANT: Davids, Andrew Robert

; APPLICANT: Pagan, Richard Joseph

; APPLICANT: Phelps, Christopher Benjamin

; APPLICANT: Power, Christine

; APPLICANT: Chvalchko, Yolande

; APPLICANT: Boeschert, Ursula

; TITLE OF INVENTION: Cytokine antagonist molecules

; FILE REFERENCE: 674582-2001

; CURRENT APPLICATION NUMBER: US/10/706,691

; PRIOR FILING DATE: 2003-11-12

; PRIOR APPLICATION NUMBER: PCT/GB03/01851

; PRIOR FILING DATE: 2003-04-30

; PRIOR APPLICATION NUMBER: GB 0209884.6

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: Seqwin9, version 1.02

; SEQ ID NO 41

; LENGTH: 416

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-706-691-41

Query Match 100.0%; Score 1205; DB 16; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.2e-101;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 MKRREGALSRSARLRLAPFYVLLLIQTDPLEGVNITSPVRLIHGTGKALLSVQYST 60
    1 MKRREGALSRSARLRLAPFYVLLLIQTDPLEGVNITSPVRLIHGTGKALLSVQYST 60
Db 1 MKRREGALSRSARLRLAPFYVLLLIQTDPLEGVNITSPVRLIHGTGKALLSVQYST 60
Qy 61 SSDRPVVMQKLRKDPVTVVOSIGTEVIGTLRPDVRDRIRLFENGSLLSLQIADDEGY 120
    61 SSDRPVVMQKLRKDPVTVVOSIGTEVIGTLRPDVRDRIRLFENGSLLSLQIADDEGY 120
Db 61 SSDRPVVMQKLRKDPVTVVOSIGTEVIGTLRPDVRDRIRLFENGSLLSLQIADDEGY 120
Qy 121 EVEISITDPTGKKTINLTVDPVISRPOVLVASTTVLESEAFLLNCSHENGTKPSYTW 180
    121 EVEISITDPTGKKTINLTVDPVISRPOVLVASTTVLESEAFLLNCSHENGTKPSYTW 180
Db 121 EVEISITDPTGKKTINLTVDPVISRPOVLVASTTVLESEAFLLNCSHENGTKPSYTW 180
Qy 181 LKDGKPLNDSRMLSPDQKVLITTRVLMEDDDLYSCWENPISQGRSLPVKITVYRRSS 240
    181 LKDGKPLNDSRMLSPDQKVLITTRVLMEDDDLYSCWENPISQGRSLPVKITVYRRSS 240
Db 181 LKDGKPLNDSRMLSPDQKVLITTRVLMEDDDLYSCWENPISQGRSLPVKITVYRRSS 240

```

RESULT 6

US-10-112-944-434

; Sequence 434, Application US/10112944

; Publication No. US20040048249A1

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Yang, Yonghong

; APPLICANT: Weng, Gezhi

; APPLICANT: Zhang, Jie

; APPLICANT: Ren, Feiyan

; APPLICANT: Xue, Aidong J.

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Wehman, Tom

; APPLICANT: Ghoesh, Malabika

; APPLICANT: Wang, Dunrui

; APPLICANT: Zhao, Qing A.

; APPLICANT: Wang, Zhiwei

; TITLE OF INVENTION: No. US20040048249A1

; SECRETED Polypeptides

; FILE REFERENCE: 805A

; CURRENT APPLICATION NUMBER: US/10/112,944

; PRIOR FILING DATE: 2002-03-28

; PRIOR APPLICATION NUMBER: US 09/488,725

; PRIOR FILING DATE: 2000-01-21

; PRIOR APPLICATION NUMBER: US 09/491,404

; PRIOR FILING DATE: 2000-01-25

; PRIOR APPLICATION NUMBER: US 09/496,914

; PRIOR FILING DATE: 2000-02-03

; PRIOR APPLICATION NUMBER: US 09/515,126

; PRIOR FILING DATE: 2000-02-28

; PRIOR APPLICATION NUMBER: US 09/519,705

; PRIOR FILING DATE: 2000-03-07

; PRIOR APPLICATION NUMBER: US 09/540,217

; PRIOR FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: US 09/552,929

; PRIOR FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: US 09/577,408

; NUMBER OF SEQ ID NOS: 924

; SOFTWARE: pc FL_genes Version 5.0

; SEQ ID NO 434

; LENGTH: 256

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-112-944-434

Query Match 97.4%; Score 1174; DB 15; Length 256;
Best Local Similarity 97.1%; Pred. No. 4.1e-99;
Matches 233; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

```

Qy 1 MKRREGALSRSARLRLAPFYVLLLIQTDPLEGVNITSPVRLIHGTGKALLSVQYST 60
    1 MKRREGALSRSARLRLAPFYVLLLIQTDPLEGVNITSPVRLIHGTGKALLSVQYST 60
Db 1 MKRREGALSRSARLRLAPFYVLLLIQTDPLEGVNITSPVRLIHGTGKALLSVQYST 60
Qy 61 SSDRPVVMQKLRKDPVTVVOSIGTEVIGTLRPDVRDRIRLFENGSLLSLQIADDEGY 120
    61 SSDRPVVMQKLRKDPVTVVOSIGTEVIGTLRPDVRDRIRLFENGSLLSLQIADDEGY 120
Db 61 SSDRPVVMQKLRKDPVTVVOSIGTEVIGTLRPDVRDRIRLFENGSLLSLQIADDEGY 120
Qy 121 EVEISITDPTGKKTINLTVDPVISRPOVLVASTTVLESEAFLLNCSHENGTKPSYTW 180
    121 EVEISITDPTGKKTINLTVDPVISRPOVLVASTTVLESEAFLLNCSHENGTKPSYTW 180
Db 121 EVEISITDPTGKKTINLTVDPVISRPOVLVASTTVLESEAFLLNCSHENGTKPSYTW 180
Qy 181 LKDGKPLNDSRMLSPDQKVLITTRVLMEDDDLYSCWENPISQGRSLPVKITVYRRSS 240
    181 LKDGKPLNDSRMLSPDQKVLITTRVLMEDDDLYSCWENPISQGRSLPVKITVYRRSS 240
Db 181 LKDGKPLNDSRMLSPDQKVLITTRVLMEDDDLYSCWENPISQGRSLPVKITVYRRSS 240

```

RESULT 7

US-10-112-944-880

; Sequence 880, Application US/10112944

; Publication No. US20040048249A1

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Yang, Yonghong

; APPLICANT: Weng, Gezhi

; APPLICANT: Zhang, Jie

; APPLICANT: Ren, Feiyan

; APPLICANT: Xue, Aidong J.

```
APPLICANT: Wang, Jian-Rui
APPLICANT: Wehrman, Tom
APPLICANT: Chosh, Malabika
APPLICANT: Wang, Dunrui
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Zhiwei
TITLE OF INVENTION: NO. US20040048249A1el Nucleic Acids and
FILE REFERENCE: 805A
CURRENT APPLICATION NUMBER: US/10/112,944
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: US 09/519,705
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 09/552,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 09/577,408
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 924
SOFTWARE: pc_fl_genes Version 5.0
SEQ ID NO 880
LENGTH: 256
TYPE: PRT
ORGANISM: Homo sapiens
US-10-112-944-880
```

```
Query Match      97.4%; Score 1174; DB 15; Length 256;
Best Local Similarity 97.1%; Pred. No. 4.1e-99;
Matches 233; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy      1 MKRREGALSRSARLARLPFYLLLIOTDPLEGNVITSPVRLIHGTGKSALLSVQYST 60
Db      1 MKRREGALSRSARLARLPFYLLLIOTDPLEGNVITSPVRLIHGTGKSALLSVQYST 60

Qy      61 SSDRPVVKMOLKRDKPYTVVQSIGTEVIGTLRPDYRDIRLFFENGSLLSDLQADEGTY 120
Db      61 SSDRPVVKMOLKRDKPYTVVQSIGTEVIGTLRPDYRDIRLFFENGSLLSDLQADEGTY 120

Qy      121 EVEISITDDTFTGEXTINLTVDPISRPQVLVASTTVLESEAFLLNCSHENGTKPSYTW 180
Db      121 EVEISITDDTFTGEXTINLTVDPISRPQVLVASTTVLESEAFLLNCSHENGTKPSYTW 180

Qy      181 LKDGKPLNDSRMLSPDQKYLITTRVLMEDDDLSCVENVPISGRSLPVKITVYRRSS 240
Db      181 LKDGKPLNDSRMLSPDQKYLITTRVLMEDDDLSCVENVPISGRSLPVKITVYRRSS 240
```

RESULT 8

```
US-10-706-691-18
Sequence 18, Application US/10706691
Publication No. US20040204352A1
GENERAL INFORMATION:
APPLICANT: Davids, Andrew Robert
APPLICANT: Pagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Power, Christine
APPLICANT: Chvatchko, Yolande
APPLICANT: Boschert, Ursula
TITLE OF INVENTION: Cytokine antagonist molecules
FILE REFERENCE: 674582-2001
CURRENT APPLICATION NUMBER: US/10/706,691
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/GB03/01851
PRIOR FILING DATE: 2003-04-30
```

```
PRIOR APPLICATION NUMBER: GB 0209884.6
PRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Seqwin99, version 1.02
SEQ ID NO 18
LENGTH: 418
TYPE: PRT
ORGANISM: Homo sapiens
US-10-706-691-18
```

```
Query Match      97.2%; Score 1171; DB 16; Length 418;
Best Local Similarity 97.5%; Pred. No. 1.5e-98;
Matches 234; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      1 MKRREGALSRSARLARLPFYLLLIOTDPLEGNVITSPVRLIHGTGKSALLSVQYST 60
Db      1 MKRREGALSRSARLARLPFYLLLIOTDPLEGNVITSPVRLIHGTGKSALLSVQYST 60

Qy      61 SSDRPVVKMOLKRDKPYTVVQSIGTEVIGTLRPDYRDIRLFFENGSLLSDLQADEGTY 120
Db      61 SSDRPVVKMOLKRDKPYTVVQSIGTEVIGTLRPDYRDIRLFFENGSLLSDLQADEGTY 120

Qy      121 EVEISITDDTFTGEXTINLTVDPISRPQVLVASTTVLESEAFLLNCSHENGTKPSYTW 180
Db      121 EVEISITDDTFTGEXTINLTVDPISRPQVLVASTTVLESEAFLLNCSHENGTKPSYTW 180

Qy      181 LKDGKPLNDSRMLSPDQKYLITTRVLMEDDDLSCVENVPISGRSLPVKITVYRRSS 240
Db      181 LKDGKPLNDSRMLSPDQKYLITTRVLMEDDDLSCVENVPISGRSLPVKITVYRRSS 240
```

RESULT 9

```
US-10-706-691-22
Sequence 22, Application US/10706691
Publication No. US20040204352A1
GENERAL INFORMATION:
APPLICANT: Davids, Andrew Robert
APPLICANT: Pagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Power, Christine
APPLICANT: Chvatchko, Yolande
APPLICANT: Boschert, Ursula
TITLE OF INVENTION: Cytokine antagonist molecules
FILE REFERENCE: 674582-2001
CURRENT APPLICATION NUMBER: US/10/706,691
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/GB03/01851
PRIOR FILING DATE: 2003-04-30
PRIOR APPLICATION NUMBER: GB 0209884.6
PRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Seqwin99, version 1.02
SEQ ID NO 22
LENGTH: 207
TYPE: PRT
ORGANISM: Homo sapiens
US-10-706-691-22
```

```
Query Match      86.7%; Score 1045; DB 16; Length 207;
Best Local Similarity 100.0%; Pred. No. 2e-87;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      34 VNITSPVRLIHGTGKSALLSVQSSSDRPVVKMOLKDKPYTVVQSIGTEVIGTLRP 93
Db      1 VNITSPVRLIHGTGKSALLSVQSSSDRPVVKMOLKDKPYTVVQSIGTEVIGTLRP 60

Qy      94 DYRDIRLFFENGSLLSDLQADEGTYEVEISITDDTFTGEXTINLTVDPISRPQVLVA 153
Db      61 DYRDIRLFFENGSLLSDLQADEGTYEVEISITDDTFTGEXTINLTVDPISRPQVLVA 120

Qy      154 STTVLESEAFLLNCSHENGTKPSYTWLKDGKPLNDSRMLSPDQKYLITTRVLMEDDD 213
Db      121 STTVLESEAFLLNCSHENGTKPSYTWLKDGKPLNDSRMLSPDQKYLITTRVLMEDDD 180
```

QY 214 LYSCHVENPISQGRSLPVKITVYRRSS 240
181 LYSCHVENPISQGRSLPVKITVYRRSS 207

RESULT 10
US-10-706-691-26

; Sequence 26, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10/706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqMan9, version 1.02
; SEQ ID NO 26
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-26

Query Match 86.7%; Score 1045; DB 16; Length 383;
Best Local Similarity 100.0%; Pred. No. 4,6e-87;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 VNITSPVRLHGTGKSAALSVQYSTSSDRPVVKQKRPVTVVQSIGTEVIGTRP 93
DB 1 VNITSPVRLHGTGKSAALSVQYSTSSDRPVVKQKRPVTVVQSIGTEVIGTRP 60
QY 94 DYRDRIRLFENGSLLSLSDQLADSGTYEVEISITDDFTGKKTINLTVDVPISRQVIVA 153
DB 61 DYRDRIRLFENGSLLSLSDQLADSGTYEVEISITDDFTGKKTINLTVDVPISRQVIVA 120
QY 154 STVLELSEAFITLNCSHENGKSTYTWLKDGPILNDSRMILSPQKVLITTRVLMEDD 213
DB 121 STVLELSEAFITLNCSHENGKSTYTWLKDGPILNDSRMILSPQKVLITTRVLMEDD 180
QY 214 LYSCHVENPISQGRSLPVKITVYRRSS 240
DB 181 LYSCHVENPISQGRSLPVKITVYRRSS 207

RESULT 11
US-10-706-691-4

; Sequence 4, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10/706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30

; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqMan9, version 1.02
; SEQ ID NO 4
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-4

Query Match 47.3%; Score 570; DB 16; Length 114;
Best Local Similarity 100.0%; Pred. No. 2,3e-44;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 PLEGVNITSPVRLHGTGKSAALSVQYSTSSDRPVVKQKRPVTVVQSIGTEVIG 89
DB 1 PLEGVNITSPVRLHGTGKSAALSVQYSTSSDRPVVKQKRPVTVVQSIGTEVIG 60
QY 90 TLRPDYRDRIRLFENGSLLSLSDQLADSGTYEVEISITDDFTGKKTINLTVDV 143
DB 61 TLRPDYRDRIRLFENGSLLSLSDQLADSGTYEVEISITDDFTGKKTINLTVDV 114

RESULT 12
US-10-706-691-24

; Sequence 24, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10/706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqMan9, version 1.02
; SEQ ID NO 24
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-24

Query Match 45.5%; Score 548; DB 16; Length 110;
Best Local Similarity 100.0%; Pred. No. 2,8e-42;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 VNITSPVRLHGTGKSAALSVQYSTSSDRPVVKQKRPVTVVQSIGTEVIGTRP 93
DB 1 VNITSPVRLHGTGKSAALSVQYSTSSDRPVVKQKRPVTVVQSIGTEVIGTRP 60
QY 94 DYRDRIRLFENGSLLSLSDQLADSGTYEVEISITDDFTGKKTINLTVDV 143
DB 61 DYRDRIRLFENGSLLSLSDQLADSGTYEVEISITDDFTGKKTINLTVDV 110

RESULT 13
US-10-706-691-6

; Sequence 6, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules

```
FILE REFERENCE: 674582-2001
CURRENT APPLICATION NUMBER: US/10/706,691
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/GB03/01851
PRIOR FILING DATE: 2003-04-30
PRIOR APPLICATION NUMBER: GB 0209884.6
PRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 43
SOFTWARE: SeqWin99, version 1.02
SEQ ID NO: 6
LENGTH: 94
TYPE: PRT
ORGANISM: Homo sapiens
US-10-706-691-6

Query Match      40.2%; Score 484; DB 16; Length 94;
Best Local Similarity 100.0%; Pred. No. 1,7e-36;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      144 PISRQVAVASTVTVLESEAFILNCSHENGKPSYTWLKDGPILNDSRMILSPDQKVL 203
Db      1 PISRQVAVASTVTVLESEAFILNCSHENGKPSYTWLKDGPILNDSRMILSPDQKVL 60

Qy      204 ITRVLMEDDDLYSCWENPISQGRSLPVKITVYR 237
Db      61 ITRVLMEDDDLYSCWENPISQGRSLPVKITVYR 94

RESULT 14
US-09-909-320-320
Sequence 320, Application US/09909320
Patent No. US20020132240A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Grimaldi, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,320
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
```

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PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO: 320
LENGTH: 450
TYPE: PRT
ORGANISM: Homo Sapien
US-09-909-320-320

Query Match      23.4%; Score 282; DB 9; Length 450;
Best Local Similarity 31.7%; Pred. No. 4.3e-17;
Matches 72; Conservative 43; Mismatches 102; Indels 10; Gaps 7;

Qy      17 LAPVYLLIQTDLLEGVNTSPVRLHGVKSAALLSVQYS--STSDRPVVKQLKR- 73
Db      3 LKVFTEFSFATGACSGKLVPSHTVHGVRGQALYFVNHGFHTPASDIOII WLPERP 61

Qy      74 -DKPVTVQSGTGVIGTGRDVRDIRLF-ENGSLILSDQLADEGTYEVEISIT--DDT 130
Db      62 HTMPRYLLGSVSKSVLPDL--EYQKFTMPPNASLLINPLQFPBEGNYIVKNIQNGT 119

Qy      131 FTGKTLINLVADVISRPOVLV-ASTVLESEAFILNCSHENGKPSYTWLKDGPILN 189
Db      120 LSAQKQIGVTVDDVTYKRVVQIHHPGSAVEYVGMNLTLCHEGSTRLAYQWLKGRPVHT 179

Qy      190 DSRMLSPDQKVLITTRVLMEDDDLYSCWENPISQGRSLPVKITVY 236
Db      180 SSTYSFSPQNNTLIHAPVTKEDIGNYSCLVNNPVSEMSDILIMPTIY 226

RESULT 15
US-09-909-088B-320
Sequence 320, Application US/09909088B
Patent No. US20020146709A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
```

APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,088B
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 320
LENGTH: 450
TYPE: PRT
ORGANISM: Homo Sapien
US-09-909-088B-320

Query Match 23.4%; Score 282; DB 9; Length 450;
Best Local Similarity 31.7%; Pred. No. 4,3e-17;
Matches 72; Conservative 43; Mismatches 102; Indels 10; Gaps 7;

QY 17 LAPFYLLIQTDPLEGVNTSPVLLINGTVGKSLLSVOYS--STSSDRPVVKWQLKR- 73
DB 3 LKVFITPLSPATGACSGLKVTVPSTHTVAGVQALYLPVHGPHRPASDIQII-WLFRFP 61
QY 74 -DKPVTVQSIGTEVYIGTLRPDYRDLRF-ENGSLLSLDIQLADEGTYEVEISIT-DDT 130
DB 62 HTPKYLIGSVKSVVPL--EYQHKFTMPMPNBSLLINPLQFPDEGNVIYKVINIQNGT 119
QY 131 FTGKTIPLTVDPVPSRPOVLY-ASTVYLLSEAFLLNCSHENGKPSYTWLKQKPLLN 189
DB 120 LSASOKIOVTVDDPVTKFVVQIHPPSGAVEYGNNTLTCHVEGGTRLAYQMLKNGRPVHT 179
QY 190 DSRMLSPDOKVLTITRYLMEDDDLVSCVENPISQGRSLPVKITVY 236

DB 180 SSTYSFSPQNTLHIAPTYKEDIGNYSCLYENPVSEMSDIIIMPLY 226

Search completed: July 26, 2005, 16:21:18
Job time : 62.4446 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 15:58:02 ; Search time 13.8684 Seconds
(without alignments)
1665.085 Million cell updates/sec

Title: US-10-706-691-20
Perfect score: 1205
Sequence: 1 MKRERGALSRRALRLAPF.....NPISQGRSLPVKITYRRSS 240

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	207.5	17.2	278	2 JCI506	biliary glycoprote
2	207.5	17.2	341	2 JCI512	biliary glycoprote
3	202.5	16.8	278	2 A39037	carcinoembryonic a
4	186	15.4	458	2 JCI509	biliary glycoprote
5	183.5	15.2	272	2 I48268	biliary glycoprote
6	183.5	15.2	629	2 A46500	LY-9.2 antigen - m
7	181	15.0	521	2 S34338	biliary glycoprote
8	179.5	14.9	278	2 JCI507	biliary glycoprote
9	179.5	14.9	341	2 JCI511	biliary glycoprote
10	178.5	14.8	475	2 A54879	pregnancy-specific
11	168.5	14.0	475	2 I76668	pregnancy-specific
12	167	13.9	853	1 IJBONC	neural cell adhesi
13	166	13.8	858	1 IJRTNC	neural cell adhesi
14	165.5	13.7	299	2 S86749	junctional adhesi
15	164	13.6	458	2 S68177	C-CAM2a protein is
16	164	13.6	458	2 S23969	cell-adhesion mole
17	164	13.6	519	2 A44783	ecto-ATPase precu
18	161	13.4	458	1 WMMSR1	biliary glycoprote
19	161	13.4	521	2 JCI508	biliary glycoprote
20	160.5	13.3	725	2 J80100	neural cell adhesi
21	160.5	13.3	1092	1 JN0635	neural cell adhesi
22	159	13.2	344	2 A27681	nonspecific cross-
23	158.5	13.2	709	2 A35364	carcinoembryonic a
24	158	13.1	321	2 JH0395	biliary glycoprote
25	158	13.1	351	2 JH0396	biliary glycoprote
26	158	13.1	417	2 JH0396	biliary glycoprote
27	158	13.1	464	2 C30127	transmembrane carc
28	158	13.1	526	1 A32164	biliary glycoprote
29	157	13.0	365	2 JCT780	coxsackie- and ade

30	156.5	13.0	761	1 IJHUNG	neural cell adhesi
31	155	12.9	324	2 G43354	pregnancy-specific
32	155	12.9	326	2 F43354	pregnancy-specific
33	155	12.9	333	2 A43354	pregnancy-specific
34	155	12.9	335	2 H43354	pregnancy-specific
35	155	12.9	395	2 D43354	pregnancy-specific
36	155	12.9	397	2 E43354	pregnancy-specific
37	155	12.9	406	2 E43354	pregnancy-specific
38	155	12.9	417	2 A28277	pregnancy-specific
39	155	12.9	419	2 A33258	pregnancy-specific
40	155	12.9	419	2 A31135	pregnancy-specific
41	155	12.9	426	2 A35964	pregnancy-specific
42	155	12.9	426	2 A33258	pregnancy-specific
43	155	12.9	426	2 A35341	pregnancy-specific
44	155	12.9	428	2 A27658	pregnancy-specific
45	154.5	12.8	725	2 J50099	neural cell adhesi

ALIGNMENTS

RESULT 1

JCI506
biliary glycoprotein B - mouse
C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C:Accession: JCI506
R:McCuai9, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
A:Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopro
A:Reference number: JCI505; MUID:93273228; PMID:8500759
A:Accession: JCI506
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-278 <MCC>
A:Cross-references: UNIPROT:Q99232
C:Comment: This protein is expressed at the cell surface and plays a determinant role in
C:Genetics:
A:Gene: BgPB
C:Superfamily: biliary glycoprotein; carcinoembryonic antigen precursor amino-terminal h
C:Keywords: glycoprotein; receptor
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F:159-216/Domain: immunoglobulin homology <IMM>
F:87,104,153,195/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	73	RDKEPTVVQSIGTEVIGTLR----	PDYRDRIRLPENGSLLLSLDLQLADEGTYEVEISITD 128
Best Local Similarity	32.1%;	Pred. No. 9.3e-09;	
Matches	54;	Conservative 32;	Mismatches 73;
		Indels 9;	Gaps 5;
Qy	73	RDKEPTVVQSIGTEVIGTLR----	PDYRDRIRLPENGSLLLSLDLQLADEGTYEVEISITD 128
Db	69	KGNPVTNAELVHOVTGNTKTTGTPAHSGRETVYNSGSLLIQRTVTKDTGYTTE--MTD 126	
Qy	129	DTF-TGSKTINLTVDVPIRPQVLVASTTVLSEAFILNCSEHENGTKPSYTLKDGKPL 187	
Db	127	ENPRTEATVQFVHQVPTQPSLQVTTNTVKEL--DSVTLTCL-SNDICANIQLFNLSQL 184	
Qy	188	LNDSRMLLSPDQKVLITITRVLMEDDDLYSCWVENPISQGRSLPVKITV 235	
Db	185	QLTERMTLSQNNILRIDPIKREDAGEYQCEISNPVSVKRSNIKLDI 232	

RESULT 2

JCI512
biliary glycoprotein H - mouse
C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C:Accession: JCI512
R:McCuai9, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
A:Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopro
A:Reference number: JCI505; MUID:93273228; PMID:8500759
A:Accession: JCI512

Db 84 TGTNTKTIK-----CPVHSGRETLVNSGLLIQRTVMKDTGVYTIE--MTDQN 128
Qy 131 F-----TGEKTNLTVDVPISRPQVLVASTVTLVLESEAFNLCSHENGTKESYTWLKDQK 185
Db 129 YRRRVLTQ-----FVHKVPQPSQVNTTIVKEL-DSVTITLCSKD-RQAHIIHWFND 182
Qy 186 PLLNDSRMLLSPDQKVLITRVLMDDDLSCMVENPISQGRSLPVKITV 235
Db 183 TLLITEKMTTQAGLILAIKIDPIKREDAGEYQCEISNPVSKRSNIKLEV 232

RESULT 6
A46500
Ly-9.2 antigen - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A46500
R:Sandrin, M.S.; Gumley, T.P.; Henning, M.M.; Vaughan, H.A.; Genez, L.J.; Trapani, J.A.; J. Immunol. 149, 1636-1641, 1992
A:Title: Isolation and characterization of cDNA clones for mouse Ly-9.
A:Reference number: A46500; MUID:92373005; PMID:1506686
A:Accession: A46500
A>Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-629 <SAN>
A:Cross-references: GB:M84412; NID:g198931; PIDN:AAA39468.1; PID:g198932
A:Experimental source: C57BL/6
A:Note: sequence extracted from NCBI backbone (NCBIN:111651, NCBIP:111654)
C:Keywords: transmembrane protein

Query Match 15.2%; Score 183.5; DB 2; Length 629;
Best Local Similarity 26.9%; Pred. No. 1.9e-06;
Matches 59; Conservative 43; Mismatches 98; Indels 19; Gaps 8;

Qy 19 PFVYLLITQDPLEGNVITSPVRLHGTGKSAVLSVQSTSDRPPVVKQLKRDKPV 78
Db 14 PLLFLM-----GLGASGKETPTVTSGLGSGVTFSLNISKDAETEHII-WNC---PPKA 65

Qy 79 VVQSIGTEVIGTLRDPYDRIRLPENG-SLLSLDLQLADEGTVEISITDDTGTGKTI 137
Db 66 LALVYFKDITLQKGYNGRLKVSDEGYSLSYNSLTKSDSGSYHAQINQKRVILTTNKEF 125

Qy 138 NLTVDPVPISRPQVLVASTVTLVLE-SEAFNLCSHENGTKPS--YTWLKDQKPLNDSRML 194
Db 126 TLHIVYKLOKQIIVSVTPSDTDSCTFLICT-VKGTQDSVQVSWTRR-----DTHLN 178

Qy 195 LSPQKVLITRVLMDDDLSCMVENPISQGRSLPVKI 233
Db 179 TYDGSHTLRVQSVCDPLPYTCRAWNPVSNQSQPVRI 217

RESULT 7
S34338
biliary glycoprotein F - mouse
N:Alternate names: mouse hepatitis virus (MHV) receptor glycoprotein
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S34338; JC1510; A41093
R:Huang, D.C.; Huang, X.F.; Novel, M.; Novel, G.
submitted to the EMBL Data Library, July 1992
A:Description: A Clp-family gene present on the lactose-protease plasmid of lactococcus
A:Reference number: S34338
A:Accession: S34338
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-521 <HUA>
A:Cross-references: UNIPROT:Q61352; EMBL:X67281; NID:g312585; PIDN:CAA47698.1; PID:g3125
R:McCuig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
A:Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopro
A:Reference number: JC1505; MUID:93273228; PMID:8500759
A:Accession: JC1510
A:Molecule type: mRNA

A:Residues: 1-81,'Q','83-141,'P',143-521 <MCC>
A:Cross-references: GB:X67281
R:Williams, R.K.; Jiang, G.S.; Holmes, K.V.
Proc. Natl. Acad. Sci. U.S.A. 88, 5533-5536, 1991
A:Title: Receptor for mouse hepatitis virus is a member of the carcinoembryonic antigen
A:Reference number: A41093; MUID:91288498; PMID:1648219
A:Accession: A41093
A>Status: preliminary
A:Molecule type: protein
A:Residues: 35-59 <Wlu>
C:Comment: This protein is expressed at the cell surface and plays a determinant role in
C:Genetics:
A:Gene: Bgpf
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal
C:Keywords: glycoprotein; receptor
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F:160-219/Domain: immunoglobulin homology <IMM1>
F:254-303/Domain: immunoglobulin homology <IMM2>
F:339-396/Domain: immunoglobulin homology <IMM3>
F:87,104,148,199,206,210,226,258,290,294,304,333,375/Binding site: carbohydrate (Asn) (c
P:87,104,148,199,206,210,226,258,290,294,304,333,375/Binding site: carbohydrate (Asn) (c

Query Match 15.0%; Score 181; DB 2; Length 521;
Best Local Similarity 27.8%; Pred. No. 2.4e-06;
Matches 47; Conservative 34; Mismatches 80; Indels 8; Gaps 4;

Qy 73 RDKPVTVQSIGTEVIGTLR---PDYDRIRLPENGSLLLSLDLQLADEGTVEISITD 128
Db 69 KGNPVSTNAEIVHFVTGNTKTTGCPAHSGRETYSNGLLIQRTVMKDTGVYTIE--MTD 126

Qy 129 DTF-TGEKTNLTVDVPISRPQVLVASTVTLVLESEAFNLCSHENGTKPSYTWLKDQK 186
Db 127 ENFRTEATVQFHVHQLLKPNTSNNPNVEGDDSVSLTCDSTDPDNITLWSRNGES 186

Qy 187 LLNDSRMLLSPDQKVLITRVLMDDDLSCMVENPISQGRSLPVKITV 235
Db 187 LSEGRKLKSEGRTLLNTRNDTGPYVCETRNPNVSNRSDPFLNI 235

RESULT 8
JC1507
biliary glycoprotein C - mouse
C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C:Accession: JC1507
R:McCuig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
A:Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopro
A:Reference number: JC1505; MUID:93273228; PMID:8500759
A:Accession: JC1507
A:Molecule type: mRNA
A:Residues: 1-278 <MCC>
A:Cross-references: UNIPROT:Q61350; GB:X67278
C:Comment: This protein is expressed at the cell surface and plays a determinant role in
C:Genetics:
A:Gene: Bgpc
C:Superfamily: biliary glycoprotein; carcinoembryonic antigen precursor amino-terminal h
C:Keywords: glycoprotein; receptor
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F:75-124/Domain: immunoglobulin homology <IMM1>
F:159-216/Domain: immunoglobulin homology <IMM2>
F:71,89,104,153,195/Binding site: carbohydrate (Asn) (covalent) #status predicted
P:71,89,104,153,195/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.9%; Score 179.5; DB 2; Length 278;
Best Local Similarity 31.7%; Pred. No. 1.4e-06;
Matches 45; Conservative 29; Mismatches 63; Indels 5; Gaps 4;

Qy 95 YDRIRLPENGSLLLSLDLQLADEGTVEISITDDTF-TGEKTNLTVDVPISRPQVLVA 153
Db 95 YSGREIYNSGLLFQMTWKMGVYTLD--WTDENYRRTQATVRFVHQVPTQPFLOVT 152

Qy 154 STTVLSEAFNLCSHENGTKPSYTWLKDQKPLNDSRMLLSPDQKVLITRVLMDDDD 213
Db 153 NTTVKEL-DSVTITLCL-SNDIGANIQLWLFNSQSLQLTERMTLSQNNISILRIDPIKREDAG 210

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Qy 214 LYSCHVENPISQGRSLPVKITV 235
Db 211 EYQCEISNPVSVRRSNSIKLDI 232

RESULT 9
JC1511
biliary glycoprotein G - mouse
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1996 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: JC1511
R;McCuaiq, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
A;Title: Expression of the Bgp gene and characterization of mouse colon biliary glycoprotein G
A;Reference number: JC1505; MUID:93273228; PMID:8500759
A;Accession: JC1511
A;Molecule type: DNA
A;Residues: 1-341 <MCC>
A;Cross-references: UNIPROT:Q61353; GB:X67282
C;Comment: This protein is expressed at the cell surface and plays a determinant role in
C;Genetics:
A;Gene: Bgpg
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: glycoprotein; receptor
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;75-124/Domain: immunoglobulin homology <IMM1>
F;159-216/Domain: immunoglobulin homology <IMM2>
F;71,89,104,153,195/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.9%; Score 179.5; DB 2; Length 341;
Best Local Similarity 31.7%; Pred. No. 1.8e-06;
Matches 45; Conservative 29; Mismatches 63; Indels 5; Gaps 4;

Qy 95 YRDRIRLFENGSLLSLDLQADEGYEVEISITDDTF-TGEKTNLTVDVPIRSPQVLVA 153
Db 95 YSGREIIYNSGLLFQMITKMDGVTYLD--MTDENYRRQTQVRFHVQPVTFEFLQVT 152

Qy 154 STTVLELSEATLNCSHENGTKPSVTWLKDGKPLNDSRMLSPDQKVLITRVLMEDDD 213
Db 153 NTVTKEL-DSVTLTCL-SNDIGANIQLFNSQSLQTLRMTLSQNSILRIDPIKREDAG 210

Qy 214 LYSCHVENPISQGRSLPVKITV 235
Db 211 EYQCEISNPVSVRRSNSIKLDI 232

RESULT 10
A54879
pregnancy-specific glycoprotein rncgm3 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C;Accession: A54879
R;Chen, H.; Chen, C.L.; Chou, J.Y.
Biochemistry 33, 9615-9626, 1994
A;Title: Characterization of two promoters of a rat pregnancy-specific glycoprotein gene
A;Reference number: A54879; MUID:94347731; PMID:8068638
A;Accession: A54879
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-475 <CHE>
A;Cross-references: UNIPROT:Q62664; GB:U09815; NID:9497254; PIDN:AAA56870.1; PID:g497255
A;Note: authors translated the codon GCT for residue 64 as Gly
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: glycoprotein
F;1-137/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA1>
F;242-378/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA2>
F;399-456/Domain: immunoglobulin homology <IMM2>

Query Match 14.8%; Score 178.5; DB 2; Length 475;
Best Local Similarity 31.5%; Pred. No. 3.3e-06;
Matches 67; Conservative 26; Mismatches 105; Indels 15; Gaps 8;

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Qy 29 DPLEGVNITSPVRLIHGTGKSALLSVQYSSTSDRPVVKW-----QLKRDKDPVTVVQSI 83
Db 269 DPTVSPLMIEPVPRAHVEGESVLLVYH--NLPEALQTSWKYGVYSLKEFK--IAEYSI 324

Qy 84 GTEVIGTLRPDYRDRIRLFPENGSLLSLDLQADEGYEVEISITDDTFGTEKTNITVDV 143
Db 325 ATKSVFP-GPAHRGRATGVNGLSLLDLQDLTARDTGLYTL-VTLDSNSKIKSAPVQVTVHK 382

Qy 144 PISRPQVLVASITV-LELSEAFTLNCSHENGTKPSVTWLKDGKPLNDSRMLSPDQKVL 202
Db 383 PVTQPFILRVTESVTVOSSVVF--CLSDN-TGVSIRLWFKNQNLQVTERMTLSPSNCQL 439

Qy 203 TITRVLMEDDDLYSCHVENPISQGRSLPVKITV 235
Db 440 RIHDVREDAGQYRCEAFNPISKTSRPPVSLAV 472

RESULT 11
I76668
pregnancy-specific glycoprotein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I76668
R;Rudert, F.; Saunders, A.M.; Thompson, J.A.; Rebstock, S.; Zimmermann, W.A.
Mamm. Genome 3, 262-273, 1992
A;Title: Characterization of murine carcinoembryonic antigen gene family members.
A;Reference number: I57007; MUID:92345715; PMID:1638085
A;Accession: I76668
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-475 <RES>
A;Cross-references: UNIPROT:Q62056; GB:M83344; NID:g200316; PIDN:AAA39916.1; PID:g200317
C;Genetics:
A;Gene: CGM5
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: glycoprotein
F;1-137/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA1>
F;399-456/Domain: immunoglobulin homology <IMM>

Query Match 14.0%; Score 168.5; DB 2; Length 475;
Best Local Similarity 28.8%; Pred. No. 1.9e-05;
Matches 70; Conservative 35; Mismatches 105; Indels 33; Gaps 11;

Qy 13 RALRLAPFVYL--LLIQTD-----PLEGVNITSPVRLIHGTGKSALLSVQYSSTSS 62
Db 243 RTLNRPRIELAHYLVQVDTLSLSCCHPLDSPQLSDPLPPHAAEGRVLLQVH--NLPE 300

Qy 63 DRPVVKWLKRDKPV--TVV-----QSIGTE--VIGTLRPDYRDRIRLFPENGSLLSLDLQ 113
Db 301 DVQTFSWY-----KGVYSTILFQIAKYSIATKSIIMGYAR---SRRETVTYNGSLLQLDVT 353

Qy 114 LADEGYEVEISITDDTFGTEKTNITVDV-PISRPQVLVASITVLELSEAFILNCSEN 172
Db 354 EKDSGVYTL---ITDTSNMGVETAHVQVNVHKLATQPVIKATDSTVRVQGSVIFTCFSDN 410

Qy 173 GTPSYTWLKGKPLNDSRMLSPDQKVLITRVLMEDDDLYSCHVENPISQGRSLPVK 232
Db 411 -TGVSIRLWFLNNORLQTLRMTLSPSKQQLWIRTVRKEDAGEYQCEAFNPVSSKTSLPVI 469

Qy 233 ITV 235
Db 470 LAV 472

RESULT 12
IJBNOC
neural cell adhesion molecule short domain form precursor - bovine
N;Alternate names: NCAM-140
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession: A32976; A38778; B44290; S05402
R;Lipkin, V.M.; Khrantsov, N.V.; Andreeva, S.G.; Moshnyakov, M.V.; Petukhova, G.V.; Raki
FEBS Lett. 254, 69-73, 1989

```

A>Title: Calmodulin-independent bovine brain adenylate cyclase. Amino acid sequence and
A/Reference number: A32976; MUID:89378239; PMID:2776887
A/Accession: A32976
A/Molecule type: mRNA
A/Residues: 1-853 <UNP>
A/Cross-references: UNIPROT:P31836; GB:X16451; NID:960; PIDN:CAA34470.1; PID:961
A/Accession: A38778
A/Molecule type: protein
A/Residues: 20-35;51-61;113-117;122-147;155-161;262-275;279-302;353-360;369-382;544-562;
A/Note: the authors identified this protein as calmodulin-independent adenylate cyclase
R/Rougou, G.; Marshak, D.R.
J. Biol. Chem. 261, 3396-3401, 1986
A/Title: Structural and immunological characterization of the amino-terminal domain of
A/Reference number: A44290; MUID:86140120; PMID:3512556
A/Accession: B44290
A/Molecule type: protein
A/Residues: 20-36 <ROU>
A/Note: 23-Glu was also found
C/Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C/Comment: Various forms of NCAM are produced by alternative splicing.
C/Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C/Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-853/Product: neural cell adhesion molecule, short domain form #status experimental
F:20-719/Domain: extracellular #status predicted <EXT>
F:34-98/Domain: immunoglobulin homology <IMM1>
F:132-191/Domain: immunoglobulin homology <IMM2>
F:152-156/Region: heparin binding #status predicted
F:161-165/Region: heparin binding #status predicted
F:228-288/Domain: immunoglobulin homology <IMM3>
F:261-270/Region: NCAM binding #status predicted
F:321-396/Domain: immunoglobulin homology <IMM4>
F:428-490/Domain: immunoglobulin homology <IMM5>
F:527-604/Domain: fibronectin type III repeat homology <FN3A>
F:633-693/Domain: fibronectin type III repeat homology <FN3B>
F:720-737/Domain: transmembrane #status predicted <TM>
F:738-853/Domain: intracellular #status predicted <INT>
F:41-96,139-189,235-286,328-394,435-488/Disulfide bonds: #status predicted
F:222,314,346,432,458,487/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.9%; Score 167; DB 1; Length 853;
Best Local Similarity 30.9%; Pred. No. 5.4e-05;
Matches 55; Conservative 28; Mismatches 7; Indels 22; Gaps 7;

Qy	61	SSDRPVVWQWKRPDPVTVVQSIGTEVIGTLRPDPYRDLRFENGSLLSLDQLADEGTY	120
Db	143	SSLPTTIWKKH-----GRDVI--LKKDV--RFVLTNNYLQIRGIKKTDEGTY	187
Qy	121	EVEISITDDTFTGKTNLTVDVP--ISRPOVLVASTTVLSEAFILNCSHENGTKPSY	178
Db	188	RCEGRILARGEINFKDIQIVNVPTVQARQSVNATA--NLGQSVTLVCNAEGFPPTV	245
Qy	179	TWLKDGKPLN--DSRMLLSPDQKVLTTIRVLMEDDDLYSCMVENPI--SQGRSLPVKI	233
Db	246	SWTKDGEIQENDEKYLFSDDSELTIRKVDKNDEAEYVCTAENKAGEQDASIHILKV	303

RESULT 13
JORTNC
neural cell adhesion molecule short domain form precursor - rat
N/Alternate names: NCAM-140
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
C/Accession: S00846; B37795; I58136
R/Small, S.J.; Shull, G.E.; Santoni, M.J.; Akeson, R.
J. Cell Biol. 105, 2335-2345, 1987
A/Title: Identification of a cDNA clone that contains the complete coding sequence for a
A/Reference number: S00846; MUID:88059265; PMID:3680385
A/Accession: S00846
A/Molecule type: mRNA
A/Residues: 1-858 <SMA>
A/Cross-references: UNIPROT:P13596; EMBL:X06564
R/Small, S.J.; Akeson, R.

J. Cell Biol. 111, 2089-2096, 1990
A/Title: Expression of the unique NCAM VASE exon is independently regulated in distinct
A/Reference number: A37795; MUID:91035620; PMID:1699951
A/Accession: B37795
A/Molecule type: mRNA
A/Residues: 340-381 <SM2>
R/Small, S.J.; Haines, S.L.; Akeson, R.A.
Neuron 1, 1007-1017, 1988
A/Title: Polypeptide variation in an N-CAM extracellular immunoglobulin-like fold is dev
A/Reference number: I58136; MUID:90166485; PMID:2483093
A/Accession: I58136
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 355-364 <RES>
A/Cross-references: GB:M32611; NID:9205643; PIDN:AAA41679.1; PID:9205644
C/Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C/Comment: Various forms of NCAM are produced by alternative splicing.
C/Genetics:
A/Gene: NCAM
C/Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C/Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-858/Product: neural cell adhesion molecule, short domain form #status predicted <MA
F:20-721/Domain: extracellular #status predicted <EXT>
F:34-98/Domain: immunoglobulin homology <IMM1>
F:132-191/Domain: immunoglobulin homology <IMM2>
F:152-156/Region: heparin binding #status predicted
F:161-165/Region: heparin binding #status predicted
F:228-290/Domain: immunoglobulin homology <IMM3>
F:263-272/Region: NCAM binding #status predicted
F:323-398/Domain: immunoglobulin homology <IMM4>
F:430-492/Domain: immunoglobulin homology <IMM5>
F:529-606/Domain: fibronectin type III repeat homology <FN3A>
F:635-695/Domain: fibronectin type III repeat homology <FN3B>
F:722-739/Domain: transmembrane #status predicted <TM>
F:740-858/Domain: intracellular #status predicted <INT>
F:41-96,139-189,235-288,330-396,437-490/Disulfide bonds: #status predicted
F:222,316,348,434,460,489/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.8%; Score 166; DB 1; Length 858;
Best Local Similarity 30.8%; Pred. No. 6.5e-05;
Matches 54; Conservative 28; Mismatches 74; Indels 24; Gaps 7;

Qy	61	SSDRPVVWQWKRPDPVTVVQSIGTEVIGTLRPDPYRDLRFENGSLLSLDQLADEGTY	120
Db	143	SSLPTTIWKKH-----GRDVI--LKKDV--RFVLSNNYLQIRGIKKTDEGTY	187
Qy	121	EVEISITDDTFTGKTNLTVDVP--ISRPOVLVASTTVLSEAFILNCSHENGTKPSY	178
Db	188	RCEGRILARGEINFKDIQIVNVPTVQARQSVNATA--NLGQSVTLVCDAFGPPEPTM	245
Qy	179	TWLKDGKPLN--DSRMLLSPDQKVLTTIRVLMEDDDLYSCMVENPI--SQGRSLPVKI	233
Db	246	SWTKDGEPIENEDDEKHIFSDSELTIRNVKNDKDEAEYVCTAENKAGEQDASIHILKV	305

RESULT 14
S56749
junctional adhesion molecule precursor - human
N/Alternate names: F11 platelet antigen; platelet adhesion molecule PAM-1; platelet F11;
C/Species: Homo sapiens (man)
C/Date: 27-Oct-1995 #sequence revision 01-Feb-2002 #text_change 09-Jul-2004
C/Accession: A59406; S56749
R/Ozaki, H.; Ishii, K.; Horiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.; K
J. Immunol. 163, 553-557, 1999
A/Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistributi
A/Reference number: A59406; MUID:99323940; PMID:10395639
A/Accession: A59406
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-299 <OZA>
A/Cross-references: UNIPROT:Q9Y624; GB:AA424050; NID:95326797; PIDN:AA424050.1

Search completed: July 26, 2005, 16:14:15
Job time : 14.8684 secs

R;Naik, U.P.; Ehrlich, Y.H.; Kornecski, E.
Biochem. J. 310, 155-162, 1995
A;Title: Mechanisms of platelet activation by a stimulatory antibody: cross-linking of a
A;Reference number: S56749; MUID:95374438; PMID:7646439
A;Accession: S56749
A;Molecule type: protein
A;Residues: 28-49,'X','51-53;62-73,'E','75-103;123,'F','125-130;'FDKDXTYLNX','LT',206,'X'
A;Note: the order of the peptides other than the amino terminus was not determined
C;Genetics:
A;Gene: JAM
C;Keywords: glycoprotein; phosphoprotein; platelet aggregation; platelet membrane
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-299/Product: junctional adhesion molecule #status predicted <MAT>

Query Match 13.7%; Score 165.5; DB 2; Length 299;
Best Local Similarity 26.2%; Pred. No. 1.8e-05;
Matches 60; Conservative 31; Mismatches 111; Indels 27; Gaps 8;

Qy 6 GALSRAGRRLAPFVYLLIOTDPLEGVNITSPVRLIHGTGKSAALLSVQYSSTSSDRP 65
Db 2 GTKAQVERKL-LCIFAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSS--P 58

Qy 66 VVKWQLKRDKEPTVVQSIGTEVI---GTLRPDYRDIRLFPENGSLLLDLQLADEGYEV 122
Db 59 RVENKFD-----QGDTTRLVCYNNKITASYEDRVTFLEPTG-ITPKSVTREDTGYTC 109

Qy 123 EISITDDTFTGKTNILTVDPISRPQVLVASTTVLESEAFTLNCSHENGTKPS-YTWL 181
Db 110 MVSEGGNSYGEVKVLIVLPSPKPTVNIPESSAT--IGNRAVLTCSEQDGSPPESEYTW 167

Qy 182 KDGKPL-----LNDSRMLSPDQKVLITRVLMEDDDLVSCMVEN 221
Db 168 KDGIVMPNPKSTRAFNSSVYLNFTTGELVDFPLSASDTGEYSCERN 216

RESULT 15
S68177
C-CAM2a protein isoform precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S68177
R;Lucka, L.; Cichocka, I.; Baemler, K.; Bechler, K.; Reutter, W.
Eur. J. Biochem. 234, 527-535, 1995
A;Title: A short isoform of carcinoembryonic-antigen-related rat liver cell-cell adhesion
A;Reference number: S68177; MUID:96128184; PMID:8536699
A;Accession: S68177
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-458 <LUC>
A;Cross-references: UNIPROT:Q63093; EMBL:X91137; NID:g1160272; PIDN:CAA62577.1; PID:g116
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
F;1-139/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA>
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-458/Product: C-CAM2a protein isoform #status predicted <MAT>
F;252-301/Domain: immunoglobulin homology <IMM>

Query Match 13.6%; Score 164; DB 2; Length 458;
Best Local Similarity 32.6%; Pred. No. 4.1e-05;
Matches 42; Conservative 24; Mismatches 61; Indels 2; Gaps 2;

Qy 107 LLLSLQLADEGTYEVEISITDDTFTGKTNILTVDPISRPQVLVASTTVLESEAFTL 166
Db 284 LFISNITNNSGTACFVNNVTGLSRTTVKNIITVFEPVQPSIQITNTTVKELG-SVTL 342

Qy 167 NCSHENGKPSYTWLKGKPLNDSRMLLSPDQKVLITRVLMEDDDLVSCMVENPISQG 226
Db 343 TCFSKD-TGVSVRWLFNSQSLQLTDRMTLSQDNSTLRIDPIKREDAGDYQCEISNPVSFR 401

Qy 227 RSLPVKITV 235
Db 402 ISHPIKLDV 410

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 15:58:52 ; Search time 17.7207 Seconds
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1011.008 Million cell updates/sec

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Perfect score: 1205
Sequence: 1 MKRRGALSRLAPLRF.....NPISQGRSLPVKITVRRSS 240

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	282	23.4	450	4	US-09-907-794A-320
2	282	23.4	450	4	Sequence 320, App
3	282	23.4	450	4	Sequence 320, App
4	282	23.4	450	4	US-09-905-125A-320
5	282	23.4	450	4	Sequence 320, App
6	282	23.4	450	4	US-09-906-700-320
7	282	23.4	450	4	Sequence 320, App
8	282	23.4	450	4	US-09-903-603A-320
9	282	23.4	450	4	Sequence 320, App
10	281	23.3	58	4	US-09-904-920A-320
11	170	14.1	316	4	US-09-513-999C-5729
12	167.5	13.9	328	4	Sequence 13, Appl
13	167.5	13.9	329	4	Sequence 6428, Ap
14	167.5	13.9	332	4	US-09-949-016-483
15	165.5	13.7	299	3	US-09-949-016-7327
16	165.5	13.7	299	3	Sequence 189, App
17	165.5	13.7	299	3	US-09-188-930-189
18	165.5	13.7	299	3	Sequence 331, App
19	165.5	13.7	299	3	US-09-462-270-2
20	165.5	13.7	299	4	US-09-254-465A-1
21	165.5	13.7	299	4	Sequence 189, App
22	165.5	13.7	299	4	US-09-312-283C-189
23	165.5	13.7	299	4	Sequence 331, App
24	165.5	13.7	299	4	US-09-312-283C-331
25	165.5	13.7	299	4	Sequence 119, App
26	165.5	13.7	299	4	US-09-907-794A-119
27	165.5	13.7	299	4	Sequence 119, App
28	165.5	13.7	299	4	US-09-905-125A-119
29	165.5	13.7	299	4	Sequence 119, App
30	165.5	13.7	299	4	US-09-902-775A-119
31	165.5	13.7	299	4	Sequence 119, App
32	165.5	13.7	299	4	US-09-902-775A-119
33	165.5	13.7	299	4	Sequence 119, App
34	165.5	13.7	299	4	US-09-397-243D-3
35	165.5	13.7	299	4	US-09-906-700-119
36	165.5	13.7	299	4	Sequence 119, App
37	165.5	13.7	299	4	US-09-903-603A-119
38	165.5	13.7	299	4	Sequence 119, App
39	165.5	13.7	299	4	US-09-904-920A-119
40	165.5	13.7	299	4	Sequence 119, App
41	165.5	13.7	299	4	US-09-905-125A-119
42	165.5	13.7	299	4	Sequence 119, App
43	165.5	13.7	299	4	US-09-906-700-119
44	165.5	13.7	299	4	Sequence 119, App
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Sequence 119, App
Sequence 119, App
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Sequence 22, Appl
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Sequence 20, Appl
Sequence 10, Appl
Sequence 12, Appl
Sequence 2, Appli
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Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-09-907-794A-320
; Sequence 320, Application US/09907794A

; Patent No. 6635468

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnovers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kijavlin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tamas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/907,794A

; CURRENT FILING DATE: 2001-07-17

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547

;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 320
;; LENGTH: 450
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-907-794A-320

Query Match 23.4%; Score 282; DB 4; Length 450;
Best Local Similarity 31.7%; Pred. No. 1.4e-19;
Matches 72; Conservative 43; Mismatches 102; Indels 10; Gaps 7;

Qy 17 LAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVOYS--STSSDRPVVKWQLKR- 73
Db 3 LKVFTTFLSPATGACGLKVTVPSTHVGVRGQALYLPVHYGHTPASDIQII-WLPERP 61

Qy 74 -DKPVTVVQSIGTEVIGTLRPDYDRIRLF-ENGSLLLSDQLADEGTYEVEISIT-DDT 130
Db 62 HTMPKYLGSVNKSVVDDL--EYQHKFTMPPPNASLLINPLQFPDEGNYIVKVNIOGNGT 119

Qy 131 FTGEKTIINTLVDPISRPQVLV-ASTTVLELSEAFNLCSHENGTKPSYTWLKDQKPLN 189
Db 120 LSASQKIQTVDVDPVKPVVQIHPGPSGAVEYVGNMTLTCHVEGTRLAYQWLKNGRPVHT 179

Qy 190 DSRMLSPDQKVLITITVLMEDDDLYSCWENPISQGRSLPVKITVY 236
Db 180 SSTYSFSPQNTLHIAPTVKEDIGNYSLVRNPVSEMESDIIMPIIY 226

RESULT 2
US-09-905-125A-320
; Sequence 320, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann

;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William, I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: 10466-14
;; CURRENT APPLICATION NUMBER: US/09/905,125A
;; CURRENT FILING DATE: 2001-07-12
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 320
;; LENGTH: 450
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-905-125A-320

Query Match 23.4%; Score 282; DB 4; Length 450;
Best Local Similarity 31.7%; Pred. No. 1.4e-19;
Matches 72; Conservative 43; Mismatches 102; Indels 10; Gaps 7;

Qy 17 LAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVOYS--STSSDRPVVKWQLKR- 73
Db 3 LKVFTTFLSPATGACGLKVTVPSTHVGVRGQALYLPVHYGHTPASDIQII-WLPERP 61

Qy 74 -DKPVTVVQSIGTEVIGTLRPDYDRIRLF-ENGSLLLSDQLADEGTYEVEISIT-DDT 130
Db 62 HTMPKYLGSVNKSVVDDL--EYQHKFTMPPPNASLLINPLQFPDEGNYIVKVNIOGNGT 119

Qy 131 FTGEKTIINTLVDPISRPQVLV-ASTTVLELSEAFNLCSHENGTKPSYTWLKDQKPLN 189
Db 120 LSASQKIQTVDVDPVKPVVQIHPGPSGAVEYVGNMTLTCHVEGTRLAYQWLKNGRPVHT 179

Qy 190 DSRMLSPDQKVLITITVLMEDDDLYSCWENPISQGRSLPVKITVY 236
Db 180 SSTYSFSPQNTLHIAPTVKEDIGNYSLVRNPVSEMESDIIMPIIY 226

RESULT 3
US-09-902-775A-320

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Query Match      23.4%; Score 282; DB 4; Length 450;
Best Local Similarity 31.7%; Pred. No. 1.4e-19;
Matches 72; Conservative 43; Mismatches 102; Indels 10; Gaps 7;

QY      17 LAPFVVLIIQTDPLEGVNITSPVRLIHGTGKSAALLSVQYS--STSSDRPVVVKWQKR- 73
Db       3 LKVFTFELSFATGACSGLKVTVPSTVHVGVGQALYLPVHYGHTPASDIQII-WLFRP 61

QY      74 -DKPVTVVOISGFEVIGTILRPDYRDIRLF-ENGSLLLSDQLADSGTYEVEISIT-DDT 130
Db       62 HTMPKYLLGSVNVKSVVVDL--EYQHKFTWMPNPASLLINPLOPDEGCVTVKVNIOQNGT 119

QY      131 FTGEKTNITVDVIPISRPQVLV-ASITVLELSEAFTLNCSHENGTKPSYTWLKDGGKPLLN 169
Db      120 LSAQKIQTIVDDPDKPVVQIHPPSGAVGYGVNMTLTCHVEGGTKRLAQWLKNGRPVHT 179

QY      190 DSRMLLSPQKVLITIRVLMEDDDLSVMENPISQGRSLPVKITVY 236
Db      180 SSTYSFSPQNNTLHIAPVKTKEDIGNYSLVRNPFVSEMSDIIMPIIY 226

RESULT 4
US-09-906-700-320
; Sequence 320, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Fan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Acids and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,700
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15

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;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 320
;; LENGTH: 450
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-906-700-320

Query Match 23.4%; Score 282; DB 4; Length 450;
Best Local Similarity 31.7%; Pred. No. 1.4e-19;
Matches 72; Conservative 43; Mismatches 102; Indels 10; Gaps 7;

Qy 17 LAPFVYLLIQTDPLEGVNITSPVRLIHGTGKSAIISVQYS--STSSDRPVVKQLKR- 73
Db 3 LKVTFITLSPATGACSLGKVTVPSTHVGVRGQALYLPVHYGFTTPASDIQII-WLPERP 61

Qy 74 -DKPVTVVQSIGTEVIGTLRPDYRDRIRLF-ENGSLLSLDLQADGTYEVEISIT-DDT 130
Db 62 HTMPKYLGSVNKSVVPDL--EYQHKFTMPPNASLLINPLQFPDEGNYIVKVNIOGNGT 119

Qy 131 FTGEKTNLTVDVPIRPOVLV-ASTTVLESEAFNLCSHENGTKPSYTWLKDGPILLN 189
Db 120 LSASQKIQTVDVDPVKPVQIHPSPGAVYVGNMTLTCHVEGTRLAYQWLKNGRPVHT 179

Qy 190 DSRMLSPDQKVLITRVLMDDDLSCVMENPISQGRSLPVKITVY 236
Db 180 SSTYSFSPQNTLHAPVTKEIDIGNYSLVRNPVSEMSDIIMPIIY 226

RESULT 5
US-09-903-603A-320
; Sequence 320, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.

;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William, I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: GNE.1618P2C12
;; CURRENT APPLICATION NUMBER: US/09/903,603A
;; CURRENT FILING DATE: 2001-07-11
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 320
;; LENGTH: 450
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-903-603A-320

Query Match 23.4%; Score 282; DB 4; Length 450;
Best Local Similarity 31.7%; Pred. No. 1.4e-19;
Matches 72; Conservative 43; Mismatches 102; Indels 10; Gaps 7;

Qy 17 LAPFVYLLIQTDPLEGVNITSPVRLIHGTGKSAIISVQYS--STSSDRPVVKQLKR- 73
Db 3 LKVTFITLSPATGACSLGKVTVPSTHVGVRGQALYLPVHYGFTTPASDIQII-WLPERP 61

Qy 74 -DKPVTVVQSIGTEVIGTLRPDYRDRIRLF-ENGSLLSLDLQADGTYEVEISIT-DDT 130
Db 62 HTMPKYLGSVNKSVVPDL--EYQHKFTMPPNASLLINPLQFPDEGNYIVKVNIOGNGT 119

Qy 131 FTGEKTNLTVDVPIRPOVLV-ASTTVLESEAFNLCSHENGTKPSYTWLKDGPILLN 189
Db 120 LSASQKIQTVDVDPVKPVQIHPSPGAVYVGNMTLTCHVEGTRLAYQWLKNGRPVHT 179

Qy 190 DSRMLSPDQKVLITRVLMDDDLSCVMENPISQGRSLPVKITVY 236
Db 180 SSTYSFSPQNTLHAPVTKEIDIGNYSLVRNPVSEMSDIIMPIIY 226

RESULT 6
US-09-904-920A-320
; Sequence 320, Application US/09904920A


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, PRIOR FILING DATE: 1999-10-05
, PRIOR APPLICATION NUMBER: PCT/US99/28214
, PRIOR FILING DATE: 1999-11-29
, PRIOR APPLICATION NUMBER: PCT/US99/28313
, PRIOR FILING DATE: 1999-11-30
, PRIOR APPLICATION NUMBER: PCT/US99/28564
, PRIOR FILING DATE: 1999-12-02
, PRIOR APPLICATION NUMBER: PCT/US99/28565
, PRIOR FILING DATE: 1999-12-02
, PRIOR APPLICATION NUMBER: PCT/US99/30095
, PRIOR FILING DATE: 1999-12-16
, PRIOR APPLICATION NUMBER: PCT/US99/30911
, PRIOR FILING DATE: 1999-12-20
, PRIOR APPLICATION NUMBER: PCT/US99/30999
, PRIOR FILING DATE: 1999-12-20
, PRIOR APPLICATION NUMBER: PCT/US00/00219
, PRIOR FILING DATE: 2000-01-05
, NUMBER OF SEQ ID NOS: 423
, SEQ ID NO 320
, LENGTH: 450
, TYPE: PRT
, ORGANISM: Homo Sapien
US-09-909-064-320

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Query Match	23.4%	Score 282;	DB 4;	Length 450;
Best Local Similarity	31.7%;	Pred. No. 1.4e-19;		
Matches	72;	Conservative 43;	Mismatches 102;	Indels 10; Gaps 7;
Qy	17	LAPFVYLLLTQTOPLEGNWITSPVRLTHGTGSKALLSVOYS--STSSDPVVKWQLKR-	73	
Db	3	LKVFTTFLSFATGACSGLKVTYSHTVHGVRGQALYLPVHYGHTPASDQIIL-WLPERP	61	
Qy	74	-DKPVTVVQSIGTEVIGTLRPDYRDRIRLF-ENGSLLLSDQLADEGTYEVEISIT--DDT	130	
Db	62	HTMPKYLKLGSVNKSVPDL--EYQHKFTMPPNASLLINLPQFDEGNYIVKVIQNGT	119	
Qy	131	FTGEKTIINLTVDVPISRPQVLV-ASTTVLSEBSAFTLNCSHENGTKPSYTWLKDGPILLN	189	
Db	120	LSASQKIQVTVDVPTKPVQIHPPSGAVEYVGNWTLTCHVEGTRLAYQWLKNGRPVHT	179	
Qy	190	DSRMLLSPDQKVLITITVLMEDDDLYSQMVENPISQGRSLPVKITVY	236	
Db	180	SSYTSFQNNLTIIAPVTKEDIGNYSCLVRNPVSEMSDIIMPIIY	226	

RESULT 8
US-09-905-381A-320
; Sequence 320, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavrin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel

```

; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,381A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 320
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-905-381A-320

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Query Match	23.4%;	Score 282;	DB 4;	Length 450;
Best Local Similarity	31.7%;	Pred. No. 1.4e-19;		
Matches	72;	Conservative 43;	Mismatches 102;	Indels 10; Gaps 7;
Qy	17	LAPFVLLLIQTDLPLGWNITSPVRLIHGVTKSALLSVQYS--STSSDPPVVKWLKR-	73	
Db	3	LKVFTTFLSPATGACSGLKVTVESHTVHVGVGQALYLPVHYGHTPASDIQII-WLFRP	61	
Qy	74	-DRPVTVVOISIGTEVIGTLRPDYDRIRLF-ENGSLLLSLQLADEGTYEVEISIT-DDT	130	
Db	62	HTMPKYLKGSVNVVVDL--EYQHKFTMPPNASLLINLPQFPDEGNYIVKVIQNGT	119	
Qy	131	FTCEKTIINLTVDPISRPQVLV-ASTTVLELSEAFITLNCSHENGTKPSYTWLKDQKPLN	189	
Db	120	LSASQIKQIVDDPVTKPVVQIHPPGGAVEYVGNMTLTCHVEGTRLAYQWLKNGRPVHT	179	
Qy	190	DSRMLLSPDQKVLITITVLMDEDDDLSCMVENPISQGRSLPVKITVY	236	
Db	180	SSYFSFSPONTLHIAPTVKEDTIGNYSCLVRNPVSEMSDIIIMPIIY	226	

RESULT 9
US-09-906-618-320
; Sequence 320, Application US/09906618
; Patent No. 6828146

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RESULT 11
US-09-397-243D-13
; Sequence 13, Application US/09397243D
; Patent No. 6695688
; GENERAL INFORMATION:
; APPLICANT: Kornecki, Elizabeth
; APPLICANT: Sobocka, Malgorzata B.
; TITLE OF INVENTION: Human Platelet F11 Receptor
; FILE REFERENCE: 011.00221
; CURRENT APPLICATION NUMBER: US/09/397,243D
; CURRENT FILING DATE: 1999-09-16
; PRIOR APPLICATION NUMBER: 60/100,638
; PRIOR FILING DATE: 1998-09-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-243D-13

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Query Match      14.1%; Score 170; DB 4; Length 316;
Best Local Similarity 24.8%; Pred. No. 1.2e-08;
Matches 58; Conservative 46; Mismatches 110; Indels 20; Gaps 11;

Qy 16 RLAPFVYLLIQTDPLEGVNITSPVRLIHGTGKALLSVQY-SSTSSDRPVVKWQKRD 74
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 KMPVLTCAVRVTVDAISVETPDVLRASQGSVTLPTCTYHTSTSSREGLIQWDKTH 63
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 75 KPVTVVSIGTEVI-GTLRPDYRDIRLFEN-----GSLLSLDLQADEGTYEVEISITD 128
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 ERVIVWPFNSKNYIHGEL---YKNRVSISNNAEQSDASITIDQLTMADNGTYECSVLSMS 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 129 DTFTGEXT-INLTVDVPIRPOVLVASTVLELSEAFTLNC-SHENGTKPSYTWLKDGP 166
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 DLEGNTKSRVRLVLPSPKPECGIEGTI--IGNNLTCTOSKEGSPFQYSKWRN-- 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 187 LLNDRMLLSP-DQKVLITITRVLMDDDLXSCMVENPISQGRSLPVKITVYRRS 239
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 177 ILNQEQLPAQSPQSVLKNISDTSGYICTSSN--EEGTQF-CNITVAVRS 227
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
US-09-949-016-6428
; Sequence 6428, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6428
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6428

Query Match      13.9%; Score 167.5; DB 4; Length 328;
Best Local Similarity 26.1%; Pred. No. 2.2e-08;
Matches 55; Conservative 40; Mismatches 93; Indels 23; Gaps 8;

Qy 20 FVYLLIQTDPLEGVNITSPVRLIHGTGKALLSVQYSSSTSSDRPVVKWQKEDKP-VT 78
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 WILLCLQTWP-EAGKDSIEFTVNGILGESVTFPVNIQEPQVK-IIAWTSKTSVAVT 64
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 79 VVQIGTEVIGTLRPDYRDIR-LFENGSLLSLDLQADEGTYEVEISITDDTFTGKTI 137
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 65 PGDETAPVTVTHRYRHALGPNVNLVISDLRMDADGYKADINTQADPYTYTKRY 124
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 138 NLTVDPVPIRPOVLVASTVLELSEAFTLNCSHENGTK-PSYTWLKDGPKLNDSRML-- 194
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 125 NLQYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKVNTYN-----SPLGEGNVLOI 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 195 -LSPDQKVLITITRVLMDDDLXSCMVENPIS 224
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 FQTPEDQELT-----YTCAQNPVS 200
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
US-09-149-476-483
; Sequence 483, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,878
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; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
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; EARLIER APPLICATION NUMBER: 60/047,594
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; EARLIER APPLICATION NUMBER: 60/047,593
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; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
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; EARLIER APPLICATION NUMBER: 60/056,664
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
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; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
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; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 13.9%; Score 167.5; DB 4; Length 329;
Best Local Similarity 26.1%; Pred. No. 2.2e-08;
Matches 55; Conservative 40; Mismatches 93; Indels 23; Gaps 8;

Qy 20 FVILLIQTDPLEGVNITSFVRLHGTGKSAALLSVQYSSSTSSDRPVVKNOLKRDKP-VT 78
Db 7 WILLLCLQWTP-EAAGKDSIFVTNGILGESVTFPVNIQEPQVK-IIAWTSTSVAYVT 64
Qy 79 VQSIGTEVIGTLRDPYDRIR-LFENGSLLLSLDLADEGTYEVEISITDDTFTGKTI 137
Db 65 PGDSETPVVTVTHRYERIHAGPNYNLVISDLRMDAGDYKADINTQADPVTTKRY 124
Qy 138 NLTVDPVIRPQVIVASTTVLESEAPTLCNSHENGTK-PSYTWLKOKGLINDSRML-- 194
Db 125 NLQIYRRLGPKITQSLMASVNSTCVTLTCSVEKEKNVTYNW----SPLGEGNVLOI 180
Qy 195 -LSPDQKVLITRVLMEDDDLSCMVENPIS 224
Db 181 FQTPDQELT-----YTCTAQNPVS 200

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US-09-949-016-7327
; Sequence 7327, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFECTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7327
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7327

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Query Match	13.9%;	Score 167.5;	DB 4;	Length 332;
Best Local Similarity	26.1%;	Pred. No. 2.2e-08;		
Matches	55;	Conservative 40;	Mismatches 93;	Indels 23; Gaps 8;
Qy	20	FVILLIQTDPLEGWNTSPVRLTHGTGKSAALLSVQYSSSTSSDRPVVVKQLKRDKP-VT	78	
Db	11	WILLLCIQTWP-EAAGKDSSEFTVNGILGESVTFPVNIQEPQVK-IIAWTSKTSVAVYT	68	
Qy	79	VVQSIGTEVIGITLPRDYRDIR-LFENGSLLSLQLADEGTYEVEISITDDTFTGKTI	137	
Db	69	PGDSEAPVVTVTHRYVYRIHALGPNYNLYISDLRMEDAGDYKADINTQADPVTTTKRY	128	
Qy	138	NLITVDVPIRRQVLVASTVTVLELSEAFPLNCSHENGTK-PSYTWLKQKGPLLNDSRML--	194	
Db	129	NLQIYRLRGKPKITQSLMASVNSTCNVTLTCSVKEEKQNTYNW-----SPLGESGNVLQI	184	
Qy	195	-LSPDQKVLITITRVLMEDEDDDLYSQWNPIS	224	
Db	185	FOTPEDEOLT-----YTCTAONFVS	204	

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RESULT 15
US-09-188-930-189
; Sequence 189, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 189
; LENGTH: 299
; TYPE: prt
; ORGANISM: Human
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (247) ... (247)
; NAME/KEY: UNSURE
; LOCATION: (289) ... (289)
US-09-188-930-189

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Query Match	13.7%;	Score 165.5;	DB 3;	Length 299;
Best Local Similarity	26.2%;	Pred.No.3e-08;		
Matches	60;	Conservative 31;	Mismatches 111;	Indels 27; Gaps 8;
Qy	6	GALSRRALRLAPFVLLLIQTDPLEGVNITSPVRLIHGTGVSALLSVQYSSTSDSRP	65	
Db	2	GTRAQVERKL-LCLFILAILLCSALGSVTVHSEPEVRIPENNPKVLSCAYSGFSS--P	58	
Qy	66	VVKQLKRDKPVTVVQSIGTEVI---GTLRPDYRDRIRLFENGSLLLSDIQLADEGTYEV	122	
Db	59	RVEWKFD-----QGDTRLVCYNNKNTASYEDRVTFELPTG-ITPKSVTREDTGTVC	109	
Qy	123	EISITDDTFTEKTIINTLVDPISRPQVLVASTTVLELSAFTLNCSCHENGTKPS--TWL	181	
Db	110	MVSEEGNSGYEVVKVILVLPSPKPTVNIPTSSAT--IGNRAVLTCSEQDGSPSEYTWTF	167	
Qy	182	KDGKPL-----LNDSRMLSPDOKVLITITRVLMDDDDLSCMVYEN	221	
Db	168	KDGLVMTPTPKSTRAFNSSVLVNPTTGEVLVDFDPLSASDTGEYSCEARN	216	

Search completed: July 26, 2005, 16:15:53
Job time : 18.7207 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2005, 15:57:23 ; Search time 98.0554 Seconds
(without alignments)
2000.159 Million cell updates/sec

Title: US-10-706-691-26
Perfect score: 1962
Sequence: 1 VNITSPVRLHGTGKSALL.....TAGVHIHQDEAGPVEISA 383

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1958	99.8	416	2 QN713	QN713 homo sapien
2	1958	99.8	416	2 Q671P8	Q671P8 homo sapien
3	1850	94.3	413	2 Q640R3	Q640R3 mus musculus
4	1318.5	67.2	367	2 Q6ZWL4	Q6ZWL4 homo sapien
5	854.5	43.6	165	2 Q6ND35	Q6ND35 homo sapien
6	268	13.7	450	2 Q6UXIO	Q6UXIO homo sapien
7	224	11.4	350	2 Q6SZ59	Q6SZ59 cercopithecus
8	219.5	11.2	351	1 C92 HUMAN	P06729 homo sapien
9	217.5	11.1	345	2 Q6SZ58	Q6SZ58 macaca aassa
10	215.5	11.0	344	2 Q6SZ62	Q6SZ62 papio anubis
11	213.5	10.9	345	2 Q6SZ63	Q6SZ63 pan troglody
12	212.5	10.8	334	2 Q6SZ56	Q6SZ56 macaca nemo
13	212.5	10.8	341	2 Q6SZ57	Q6SZ57 macaca arct
14	211	10.8	341	2 Q61354	Q61354 mus musculus
15	210.5	10.7	351	2 Q6SZ61	Q6SZ61 macaca fasc
16	207.5	10.6	351	2 Q6SZ60	Q6SZ60 macaca mula
17	206.5	10.5	292	2 Q6UY47	Q6UY47 homo sapien
18	202.5	10.3	278	2 Q99232	Q99232 mus musculus
19	199.5	10.2	1093	1 LFG1 HUMAN	Q96JAI homo sapien
20	198.5	10.1	340	2 Q61349	Q61349 mus musculus
21	196.5	10.0	387	2 Q6EXK7	Q6EXK7 homo sapien
22	186.5	10.0	412	2 Q6MZS4	Q6MZS4 homo sapien
23	189.5	9.7	319	1 A33 HUMAN	Q99795 homo sapien
24	189	9.6	365	2 Q6WMV3	Q6WMV3 bos taurus
25	188.5	9.6	1091	1 LFG1 MOUSE	P70193 mus musculus
26	187.5	9.6	325	2 Q95791	Q95791 homo sapien
27	186	9.5	337	2 P97268	P97268 cavia porce
28	186	9.5	341	2 Q61353	Q61353 mus musculus
29	185.5	9.5	235	2 Q75296	Q75296 homo sapien
30	185.5	9.5	327	2 Q96107	Q96107 homo sapien
31	185	9.4	272	2 Q9R1N5	Q9R1N5 mus musculus

Q9R067 rattus norv
Q9R066 rattus norv
P78310 homo sapien
Q91W66 mus musculus
P97792 mus musculus
Q9dbj8 mus musculus
Q9ukv4 mus musculus
Q9cva4 mus musculus
Q9jhl7 rattus norv
Q91351 mus musculus
Q61352 mus musculus
Q6VAN5 bos taurus
Q6VAN6 bos taurus
Q6VAN7 bos taurus

ALIGNMENTS

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RESULT 1
QN713
ID QN713 PRELIMINARY; PRT; 416 AA.
AC QN713;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ25530.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
RA Nagai K., Isegai T., Sugano S.,
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK098396; BAC05297.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 416 AA; 45994 MW; 47120CA9A00EE1CF CRC64;
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Query Match 99.8%; Score 1958; DB 2; Length 416;
Best Local Similarity 99.7%; Pred. No. 3.3e-106;
Matches 382; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VNITSPVRLHGTGKSALLSVQYSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 60
Db 34 VNITSPVRLHGTGKSALLSVQYSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 93
Qy 61 DYDRIRLFPENGSLISDLQADEGTYVEISITDDTFTGKTNILTVDPISRPVLVA 120
Db 94 DYDRIRLFPENGSLISDLQADEGTYVEISITDDTFTGKTNILTVDPISRPVLVA 153
Qy 121 STTVLESEAFNLCSHENGTKFSYTWLKGKPLNDSRMLLSPDQKVLITRVLMEDDD 180
Db 154 STTVLESEAFNLCSHENGTKFSYTWLKGKPLNDSRMLLSPDQKVLITRVLMEDDD 213
Qy 181 LYSQWVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLTVCAWCKPSKRKQKCL 240
Db 214 LYSQWVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLTVCAWCKPSKRKQKCL 273
Qy 241 EKQNSLEYMDQNDRLKPEADTLPRSGEQERKNPMALYILKDKDSPTEENPAPEPSAT 300
Db 274 EKQNSLEYMDQNDRLKPEADTLPRSGEQERKNPMALYILKDKDSPTEENPAPEPSAT 333
Qy 301 EPGPGYSVSPVGRSPGLPIRSARRYPRSPARSPATGRTHSSPPRPSPSSPGRSRASR 360
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Db 334 EPGPGYVSVPVGRSPGLPIRSARYPRSPARSPATGRTHSSPPAPSPGRSASR 393
Qy 361 TLRTAGVHIIREQEAGPVEISA 383
Db 394 TLRTAGVHIIREQEAGPVEISA 416

RESULT 2
Q67IP8 PRELIMINARY; PRT; 416 AA.
AC Q67IP8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Shen S., Moh M.C.;
RT "A gene related to human hepatocellular carcinoma.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY047587; AAQ0308.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG: 1.
DR SMART; SM00409; IG: 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Hypothetical protein.
SQ SEQUENCE 416 AA; 46055 MW; 788882298BEB4ABF CRC64;

Query Match 99.8%; Score 1959; DB 2; Length 416;
Best Local Similarity 99.7%; Pred. No. 3.3e-106;
Matches 382; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNITSPVRLIHGTGKSGALLSVQYSTSSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 60
Db 34 VNITSPVRLIHGTGKSGALLSVQYSTSSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 93
Qy 61 DYDRIRLRFENGSLLLSDQLADSGTYEVEISITDDTFTGKTNLTVDVPISRPQVLVA 120
Db 94 DYDRIRLRFENGSLLLSDQLADSGTYEVEISITDDTFTGKTNLTVDVPISRPQVLVA 153
Qy 121 STTVLELSEAFNLCSHENGTKPSYTWLKDGPILLNDSRMLSPDQKVLITITRVLMEDDD 180
Db 154 STTVLELSEAFNLCSHENGTKPSYTWLKDGPILLNDSRMLSPDQKVLITITRVLMEDDD 213
Qy 181 LYSQWENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLTVCAWKPSKQKQL 240
Db 214 LYSQWENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLTVCAWKPSKQKQL 273
Qy 241 EKQNSLEYMDQNDRLKPEATLPRSGEQRKNPMALYILKDKOSPTEENPAPEPSAT 300
Db 274 EKQNSLEYMDQNDRLKPEATLPRSGEQRKNPMALYILKDKOSPTEENPAPEPSAT 333
Qy 301 EPGPGYVSVPVGRSPGLPIRSARYPRSPARSPATGRTHSSPPAPSPGRSASR 360
Db 334 EPGPGYVSVPVGRSPGLPIRSARYPRSPARSPATGRTHSSPPAPSPGRSASR 393
Qy 361 TLRTAGVHIIREQEAGPVEISA 383
Db 394 TLRTAGVHIIREQEAGPVEISA 416

RESULT 3
Q640R3 PRELIMINARY; PRT; 413 AA.
ID Q640R3
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AC Q640R3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 2900042E01RIK protein (Fragment).
GN Name=2900042E01RIK;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Moore T., Max S.I., Wang J., Hulyk S.W.,
RA Hopkins R.F., Jordan H., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Srapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Director MGC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC082537; AAH82537.1; -.
FT NON TER 1
SQ SEQUENCE 413 AA; 45665 MW; B6EFCAD2D6D2CA3C1 CRC64;

Query Match 94.3%; Score 1850; DB 2; Length 413;
Best Local Similarity 94.5%; Pred. No. 6.4e-100;
Matches 364; Conservative 9; Mismatches 10; Indels 2; Gaps 1;

Qy 1 VNITSPVRLIHGTGKSGALLSVQYSTSSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 60
Db 29 VNITSPVRLIHGTGKSGALLSVQYSTSSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 88
Qy 61 DYDRIRLRFENGSLLLSDQLADSGTYEVEISITDDTFTGKTNLTVDVPISRPQVLVA 120
Db 89 DYDRIRLRFENGSLLLSDQLADSGTYEVEISITDDTFTGKTNLTVDVPISRPQVLVA 148
Qy 121 STTVLELSEAFNLCSHENGTKPSYTWLKDGPILLNDSRMLSPDQKVLITITRVLMEDDD 180
Db 149 STTVLELSEAFNLCSHENGTKPSYTWLKDGPILLNDSRMLSPDQKVLITITRVLMEDDD 208
Qy 181 LYSQWENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLTVCAWKPSK--RKQK 238
Db 209 LYSQWENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLTVCAWKPSKSKRKR 268
Qy 239 KLEKQNSLEYMDQNDRLKPEATLPRSGEQRKNPMALYILKDKOSPTEENPAPEPS 298
Db 269 KLEKQNSLEYMDQNDRLKPEATLPRSGEQRKNPMALYILKDKOSPTEENPAPEPS 328
Qy 299 ATEPGPGYVSVPVGRSPGLPIRSARYPRSPARSPATGRTHSSPPAPSPGRSASR 358
Db 329 TTEPGPGYVSVPVGRSPGLPIRSARYPRSPARSPATGRTHSSPPAPSPGRSASR 388
Qy 359 SRTLRTAGVHIIREQEAGPVEISA 383
||:||||| |||||:|||||
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Db 389 SRSRLTAGVQRIRQESQGVVEISA 413
RESULT 4
Q6ZWL4
ID Q6ZWL4 PRELIMINARY; PRT; 367 AA.
AC Q6ZWL4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ16002.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Suzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Shiohata N.,
RA Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,
RA Matsumura Y., Moriya S., Chiba E., Momiyama H., Onogawa S.,
RA Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Kataoka R.,
RA Kuga N., Kuroda A., Satoh I., Kanata K., Takami S., Terashima Y.,
RA Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T.,
RA Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K.,
RA Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y.,
RA Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.,
RA Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK122595; BAC85486.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR DR
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 2.
DR DR
DR PROSITE; PS50835; IG_LIKE; 1.
DR Receptor.
KW RECEPTOR.
SQ SEQUENCE 367 AA; 40456 MW; 35956FA245A408F0 CRC64;
Query Match 67.2%; Score 1318.5; DB 2; Length 367;
Best Local Similarity 83.2%; Pred. No. 4.9e-69;
Matches 272; Conservative 12; Mismatches 26; Indels 17; Gaps 4;
Qy 1 VNITSPVRLHGTGKSGALLSVQISSTSSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 60
Db 34 VNITSPVRLHGTGKSGALLSVQISSTSSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 93
Qy 61 DYDRIRLRFENGSLLSLDQLADSGTYEVEISITDDTFTGKTLNLTVDVPIRPOVLVA 120
Db 94 DSDRIRLRFENGSLLSLDQLADSGTYEVEISITDDTFTGKTLNLTVDVPIRPOVLVA 153
Qy 121 STTVLELSEAFNLCSHENGTKPSYTWLKGKPLNDSRMLSPDQKVLITRIVLMEDDDD 180
Db 154 STTVLELSEAFNLCSHENGTKPSYTWLKGKPLNDSRMLSPDQKVLITRIVLMEDDDD 213
Qy 181 LYSQWENPISQGRSLPVKITYRRSSLIYILSTGGIFLLVTLTVTCACWKPSKRRKKKL 240
Db 214 LYSQWENPISQGRSLPVKITYRRSSLIYILSTGGIFLLVTLTVTCACWKPSKRRKKKL 273
Qy 241 EKQNSLEYMDNDRLKPEADTLPRSGEQRKNPMALYI-----LKQDPSPTEE 290
Db 274 EKQNSLEYMDNDRLKPEGE-LPAT-----QSPITSRISVGKWEKAEIGDKENSAGT 327
Qy 291 NPAPPEPS-ATEPGPGYSVPVPGR 316
Db 328 LPSDLGASKGKEPFASLSHSLPR 354
RESULT 5
Q8ND35
ID Q8ND35 PRELIMINARY; PRT; 165 AA.
AC Q8ND35;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein DKF2p5470159 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Bloeker H., Boecher M., Brandt P., Mewes H.W., Weil B., Wiemann S.;
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AL834419; CAD39081.1; -.
DR EMBL; AL834419; CAD39081.1; -.
DR KW Hypothetical protein.
SQ SEQUENCE 165 AA; 18161 MW; 5052FA978C437486 CRC64;
Query Match 43.6%; Score 854.5; DB 2; Length 165;
Best Local Similarity 99.4%; Pred. No. 1.9e-42;
Matches 165; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 218 FLVTLTVTCACWKPSKRRKKLEKQNSLEYMDNDRLKPEADTLPRSGEQRKNPMAL 277
Db 1 FLVTLTVTCACWKPSKRRKKLEKQNSLEYMDNDRLKPE-DTLPRSGEQRKNPMAL 59
Qy 278 YILKQDPSPTENPAPEPSRATPGPGYSVPVPGRSGPLPIRSARYPRSPARSPA 337
Db 60 YILKQDPSPTENPAPEPSRATPGPGYSVPVPGRSGPLPIRSARYPRSPARSPA 119
Qy 338 TGRTHSSPPRAPSPGSRASRTLRAGVHIIRQDEAGPVEISA 383
Db 120 TGRTHSSPPRAPSPGSRASRTLRAGVHIIRQDEAGPVEISA 165
RESULT 6
Q6UXIO
ID Q6UXIO PRELIMINARY; PRT; 450 AA.
AC Q6UXIO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE WLKV305.
GN ORFNames=UNQ305;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.
RA "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358345; AAQ88711.1; -.
DR InterPro; IPR003598; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 3.
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DR SMART: SM00408; IGC2; 1.
DR PROSITE: PS00835; IG LIKE; 2.
SQ SEQUENCE 450 AA; 50114 MW; A22FF822CC3CB226 CRC64;

Query Match 13.7%; Score 268; DB 2; Length 450;
Best Local Similarity 31.9%; Pred. No. 9.3e-08;
Matches 67; Conservative 43; Mismatches 90; Indels 10; Gaps 7;

Qy 1 VNITSPVRLHGTGKSAALLSVQYS--STSDRPVVKWQLKR--DKPVTVVQSGTGTGVIG 56
Db 20 LKVTVPSTHVGVRGQALYLPVHYGFHTPASDIQII-WLFRPHTMPKYLGLSVNKSVP 78
Qy 57 TLRPDYDRIRLP-ENGLSLLSLDLQADGTYEVEISIT-DDTFTGKTNILNLTVDVPISR 114
Db 79 DL--EYQHKFTMPNPASLLINLPQFPDEGNIYVKVNIQNGTSLASQKQVTVDDPVTK 136
Qy 115 PQVLV-ASTVTLELSEAFTHLNCSHENGTPKPSYTWLKDGPILLNDSRMLLSPDQKVLITR 173
Db 137 PVQIHPPSGAVEYVGNMNTLTCHVEGGTRLAYQMLKNGRPVHTSSTYSFSPQNTLHAP 196
Qy 174 VLMEDDLISYCMWENPISQGRSLPVKITVY 203
Db 197 VTKEIDIGNYSCLVRNPVSEMSDIIMPIY 226

RESULT 7
ID Q6S259 PRELIMINARY; PRT; 350 AA.
AC Q6S259;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cluster of differentiation 2.
GN Name=CD2;
OS Cercopithecus torquatus atys (Red-crowned mangabey) (sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15302161;
RA Dameschroder M.M., Kozhich A.A., Woods R.M., Cheng L., Mullikin B.A.,
RA Wilson S.D., Ulbrandt N.D., Bachy C.M., Wu H., Suzich J.A.,
RA Kiener P.A., Dall'Acqua W.F., White W.I.;
RT "Analysis of human and primate CD2 molecules by protein sequence and
RT epitope mapping with anti-human CD2 antibodies.";
RL Mol. Immunol. 41:985-1000(2004).
DR EMBL; AY445038; AAR15885.1; -.
DR HSP; P08921; I464
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008424; CD2.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF05790; C2-set; 1.
SQ SEQUENCE 350 AA; 39493 MW; 621C74BC81D8C95D CRC64;

Query Match 11.4%; Score 224; DB 2; Length 350;
Best Local Similarity 23.5%; Pred. No. 2.5e-05;
Matches 84; Conservative 61; Mismatches 146; Indels 66; Gaps 13;

Qy 12 GTVGSALLSVQYSSTSDRPVVKWQLKRDKPVTVVQSGTGTGVIGTLRP---DYRDRIR 67
Db 35 GALGQDIDIDIPSFQMSODIDIRWEKTSK-----KKIAQFRKEKTFEKKYK 84
Qy 68 LPENGSLLSLDLQADGTYEVEISITDDTFTGKTNILNLTVDVPISRQVLVASTVLEL 127
Db 85 LFKNGTLKILKIHQDQSYKVIYDTNGKNVLEKTFDLKIGERYSKPKI---SWTCINT 141
Qy 128 SFAFTLNCSEHNGTPKPSYTWLKDGPILLNDSRMLLSPDQKVLITRVLMEDDLISYC 184
Db 142 ----TLICEVMNGTDPNLNYQDGKH-----LKLQRVITHKWTNLSAK----PKC 185

Qy 185 MVENPISQGRSLPVKITVYRRSSLYIILS-TGGIFLLVTLVTVCAWKPCKRKKLEKQ 243
Db 186 TAGNKVSKESRVTCTEKGLDILYIIGICGGSLLVFVTLVVFVITKTKQRS----- 241
Qy 244 NSLEYWDQNDRLKPEADTLPRSGEGRKNPMALYILKDKDSPETENPAPERPSATE-- 301
Db 242 -----RRNDEELEIRAH---RAATEERGRKPHQIPASTPQNPAASQHPPPPPGHR 292
Qy 302 ---PGPGYSVS-----PAVPG---RSPGPIRSARRYPSPARSPARTGTHSS 344
Db 293 SHRLPPGHRVQHQPAPSPAPSGTQVHQKGPPLPRVQPKPPQQAENSLSPPSS 349

RESULT 8
ID CD2_HUMAN STANDARD; PRT; 351 AA.
AC P06729; Q96TE5;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE T-cell surface antigen CD2 precursor (T-cell surface antigen T11/Leu-
DE S) (LFA-2) (LFA-3 receptor) (Erythrocyte receptor) (Rosette receptor).
GN Name=CD2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT HIS-266.
RX MEDLINE=88144486; PubMed=2894031;
RA Diamond D.J., Clayton L.K., Sayre P.H., Reinherz E.L.;
RT "Exon-intron organization and sequence comparison of human and murine
RT T11 (CD2) genes";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1615-1619(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87204137; PubMed=2437578;
RA Seed B., Aruffo A.;
RT "Molecular cloning of the CD2 antigen, the T-cell erythrocyte
RT receptor, by a rapid immunoselection procedure.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:3365-3369(1987).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT HIS-266.
RX MEDLINE=87041523; PubMed=3490670;
RA Sewell W.A., Brown M.H., Dunne J., Owen M.J., Crumpton M.J.;
RT "Molecular cloning of the human T-lymphocyte surface CD2 (T11
RT antigen.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:8718-8722(1986).
RN [4]
RP REVISIONS.
RA Sewell W.A., Brown M.H., Dunne J., Owen M.J., Crumpton M.J.;
RL Proc. Natl. Acad. Sci. U.S.A. 84:7256-7256(1987).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=87204243; PubMed=2883656;
RA Sayre P.H., Chang H.-C., Hussey R.E., Brown N.R., Richardson N.E.,
RA Spagnoli G., Clayton L.K., Reinherz E.L.;
RT "Molecular cloning and expression of T11 cDNAs reveal a receptor-like
RT structure on human T lymphocytes.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:2941-2945(1987).
RN [6]
RP SEQUENCE FROM N.A., AND VARIANT HIS-266.
RX MEDLINE=89005055; PubMed=2901953;
RA Lang G., Wotton D., Owen M.J., Sewell W.A., Brown M.H., Mason D.Y.,
RA Crumpton M.J., Kioussis D.;
RT "The structure of the human CD2 gene and its expression in transgenic
RT mice.";
RL EMBO J. 7:1675-1682(1988).
RN [7]
RP SEQUENCE FROM N.A., AND VARIANT HIS-266.
RA Hall R.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [8]
```

RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas, and Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 25-206.
RX MEDLINE=95086863; PubMed=7994575;
RA Bodian D.L., Jones E.Y., Harlos K., Stuart D.I., Davis S.J.;
RT "Crystal structure of the extracellular region of the human cell
RT adhesion molecule CD2 at 2.5-A resolution.";
RL Structure 2:755-766 (1994).
RN [10]
RP STRUCTURE BY NMR OF 25-129.
RX MEDLINE=94348865; PubMed=7915183; DOI=10.1016/0969-2126(93)90009-6;
RA Withka J.M., Wyss D.F., Wagner G., Arulanandam A.R.N., Reinherz E.L.,
RA Reeney M.A.;
RT "Structure of the glycosylated adhesion domain of human T lymphocyte
RT glycoprotein CD2.";
RL Structure 1:69-81 (1993).
RN [11]
RP STRUCTURE BY NMR OF 25-129.
RX MEDLINE=95381065; PubMed=7544493;
RA Wyss D.F., Choi J.S., Li J., Knoppers M.H., Willis K.J.,
RA Arulanandam A.R., Smolyar A., Reinherz E.L., Wagner G.;
RT "Conformation and function of the N-linked glycan in the adhesion
RT domain of human CD2.";
RL Science 269:1273-1278 (1995).
RN [12]
RP MUTAGENESIS.
RX MEDLINE=88039075; PubMed=2444890; DOI=10.1038/329842a0;
RA Peterson A., Seed B.;
RT "Monoclonal antibody and ligand binding sites of the T cell
RT erythrocyte receptor (CD2).";
RL Nature 329:842-846 (1987).
RN [13]
RP CD59-BINDING DATA.
RX MEDLINE=92311658; PubMed=1377404;
RA Hahn W.C., Menu E., Rothwell A.L.M., Sims P.J., Bierer B.E.;
RT "Overlapping but nonidentical binding sites on CD2 for CD58 and a
RT second ligand CD59.";
RL Science 256:1805-1807 (1992).
CC -!- FUNCTION: CD2 interacts with lymphocyte function-associated
CC antigen (LFA-3) and CD48/ICAM1 to mediate adhesion between T cells
CC and other cell types. CD2 is implicated in the triggering of T-
CC cells, the cytoplasmic domain is implicated in the signaling
CC function.
CC -!- SUBUNIT: Interacts with CD2AP (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- DATABASE: NAME=PROV; NOTE=CD guide CD2 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd2.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M16445; AAA51738.1; -;
DR EMBL; M14362; AAA35571.1; -;
DR EMBL; M16336; AAA51946.1; -;
DR EMBL; M19806; AAA53095.1; -;
DR EMBL; M19798; AAA53095.1; JOINED.
DR EMBL; M19800; AAA53095.1; JOINED.
DR EMBL; M19802; AAA53095.1; JOINED.
DR EMBL; M19804; AAA53095.1; JOINED.
DR EMBL; X07871; CAA30721.1; -;
DR EMBL; X07872; CAA30721.1; JOINED.
DR EMBL; X07873; CAA30721.1; JOINED.
DR EMBL; X07874; CAA30721.1; JOINED.
DR EMBL; AL135798; CAC14840.1; -;
DR EMBL; AC033583; AAH33583.1; -;
DR PIR; A28967; RWIUC2.
DR PDB; 1CDB; NMR; @=25-129.
DR PDB; 1GYA; NMR; @=25-129.
DR PDB; 1HNF; X-ray; @=25-206.
DR PDB; 1L2Z; NMR; B=294-304.
DR GlycoSuiteDB; P06729; -;
DR Genew; HGNC:1639; CD2.
DR H-InvDB; HIX0000931; -;
DR MM; 186990; -;
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0005515; P:protein binding; IPI.
DR GO; GO:0004872; P:receptor activity; NAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
DR GO; GO:0016337; P:cell-cell adhesion; NAS.
DR GO; GO:0006917; P:induction of apoptosis; TAS.
DR GO; GO:0001766; P:lipid raft polarization; TAS.
DR GO; GO:0031011; P:natural killer cell activation; NAS.
DR GO; GO:0030887; P:positive regulation of dendritic cell activ. .; NAS.
DR GO; GO:0045580; P:regulation of T-cell differentiation; NAS.
DR GO; GO:0042110; P:T-cell activation; TAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF05790; CD2; 1.
DR PROSITE; PS00835; IG_LIKE; FALSE_NEG.
DR 3D-structure; Antigen; Cell adhesion; Glycoprotein;
KW Immunoglobulin domain; Polymorphism; Repeat; Signal; T-cell;
KW Transmembrane.
KW SIGNAL 1 24 T-cell surface antigen CD2.
FT CHAIN 25 351 Extracellular (Potential).
FT DOMAIN 25 209 Potential.
FT TRANSMEM 210 235 Cytoplasmic (Potential).
FT DOMAIN 236 351 IG-like V-type.
FT DOMAIN 25 128 IG-like C2-type.
FT DOMAIN 129 209 LFA-3 (CD58) binding region 1.
FT DOMAIN 61 75 LFA-3 (CD58) binding region 2.
FT DOMAIN 106 120 Pro-rich.
FT DOMAIN 282 338 By similarity.
FT DISULFID 139 203 By similarity.
FT DISULFID 146 186 N-linked (GlcNAc. . .).
FT CARBOHYD 89 89 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 141 141 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 150 150 Q->H (in dSNP:699738).
FT VARIANT 266 266 /FTID=VAR_017104.
FT MUTAGEN 67 67 K->R: Loss of LFA-3 binding.
FT MUTAGEN 70 70 Q->K: Loss of LFA-3 binding.
FT MUTAGEN 110 110 Y->D: Loss of LFA-3 and CD59 binding.
FT MUTAGEN 111 111 D->H: Loss of LFA-3 and CD59 binding.
Query Match 11.2%; Score 219.5; DB 1; Length 351;
Best Local Similarity 23.6%; Pred. No. 4.6e-05;
Matches 81; Conservative 53; Mismatches 148; Indels 61; Gaps 11;

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QY 12 GTVGSALLSVQYSSTSSDRPVVWQKRDKPVTVVQSIGTEVIGTLRPD-----YRDRI 66
Db 35 GALGQDINLIPSFQMSDDDDIKWETSDK-----KKIAQFRKEKETEFEKD Y 84
QY 67 RLFEKNGSLLSLDLQADAGTYEVEISITDDTFTGKNTINLTVDPISRPQVLVASTTVLE 126
Db 85 KLFKNGTLKIKHLKHDDQDSYKVSIDYTKGNVLEKIFDLKIQERVSKPKI---SWTCIN 141
QY 127 LSEAFNLCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDDDLVSCMW 186
Db 142 T-----TLTCEVMNGTDPNLNYQDGKHLKLSQRVITHKWTTSLSAK-----FKCTA 188
QY 187 ENPISQGRSLPVKITVYRRSSLYIILS-TGGIFLLVTLTVTCACWKPSKRKOKKLEKQNS 245
Db 189 GNKVSKESSMETVSCPEKGLDIYLIIGICGGSLLMVFVALLVFIYITKRKKQRS-----242
QY 246 LEYMDQNDRLKPEADTLPRSGEQRKNPMALYILKDKSPETENPAPRPSATE-----301
Db 243 -----QRNDEELETRAH---RVATEERGRKPHQIPASTPQNPAAHQPPPPGHRSQAPSH 295
QY 302 -PGPPGYSVS-----PAVPG-----RSPGLPIRSARRYPRSP 332
Db 296 RPLPPGHRVQHQPQRPPAPSGTQVHQKGPPLPRPRVQPKPP 338

RESULT 9
Q6S258 PRELIMINARY; PRT; 345 AA.
AC Q6S258;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Cluster of differentiation 2 (Fragment).
GN Name=CD2;
OS Macaca assamensis (Assam's macaque) (Assam's monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciae;
OC Cercopitheciae; Macaca.
OX NCBI_TaxID=9551;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15302161;
RA Damschroder M.M., Kozhich A.A., Woods R.M., Cheng L., Mullikin B.A.,
RA Wilson S.D., Ulbrandt N.D., Bachy C.M., Wu H., Suzich J.A.,
RA Kiener P.A., Dall'Acqua W.F., White W.I.;
RT "Analysis of human and primate CD2 molecules by protein sequence and
RT epitope mapping with anti-human CD2 antibodies.";
RL Mol. Immunol. 41:985-1000(2004).
DR EMBL; AY445039; AAR15886.1; -
DR HSP; P08921; I464.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008424; CD2.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF05790; C2-set; 1.
FT NON_TER 345 345
SQ SEQUENCE 345 AA; 38952 MW; 063DF110344542A7 CRC64;

Query Match 11.1%; Score 217.5; DB 2; Length 345;
Best Local Similarity 23.3%; Pred. No. 5.9e-05;
Matches 80; Conservative 54; Mismatches 148; Indels 61; Gaps 11;

QY 12 GTVGSALLSVQYSSTSSDRPVVWQKRDKPVTVVQSIGTEVIGTLRPD-----YRDRI 66
Db 35 GALGQDINLIPSFQMSDDDDIKWETSDK-----KKIAQFRKEKETEFEKD Y 84
QY 67 RLFEKNGSLLSLDLQADAGTYEVEISITDDTFTGKNTINLTVDPISRPQVLVASTTVLE 126
Db 85 KLFKNGTLKIKHLKHDDQDSYKVSIDYTKGNVLEKIFDLKIQERVSKPKI---SWTCIN 141
QY 127 LSEAFNLCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDDDLVSCMW 186
Db 142 T-----TLTCEVMNGTDPNLNYQDGKHLKLSQRVITHKWTTSLSAK-----FKCTA 188
QY 187 ENPISQGRSLPVKITVYRRSSLYIILS-TGGIFLLVTLTVTCACWKPSKRKOKKLEKQNS 245
Db 189 GNKVSKESSMETVSCPEKGLDIYLIIGICGGSLLMVFVALLVFIYITKRKKQRS-----242
QY 246 LEYMDQNDRLKPEADTLPRSGEQRKNPMALYILKDKSPETENPAPRPSATE-----301
Db 243 -----QRNDEELETRAH---RVATEERGRKPHQIPASTPQNPAAHQPPPPGHRSQAPSH 295
QY 302 -PGPPGYSVS-----PAVPG-----RSPGLPIRSARRYPRSP 332
Db 296 RPLPPGHRVQHQPQRPPAPSGTQVHQKGPPLPRPRVQPKPP 338

RESULT 9
Q6S262 PRELIMINARY; PRT; 344 AA.
AC Q6S262;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Cluster of differentiation 2 (Fragment).
GN Name=CD2;
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciae;
OC Cercopitheciae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15302161;
RA Damschroder M.M., Kozhich A.A., Woods R.M., Cheng L., Mullikin B.A.,
RA Wilson S.D., Ulbrandt N.D., Bachy C.M., Wu H., Suzich J.A.,
RA Kiener P.A., Dall'Acqua W.F., White W.I.;
RT "Analysis of human and primate CD2 molecules by protein sequence and
RT epitope mapping with anti-human CD2 antibodies.";
RL Mol. Immunol. 41:985-1000(2004).
DR EMBL; AY445035; AAR15882.1; -
DR HSP; P08921; I464.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008424; CD2.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF05790; C2-set; 1.
FT NON_TER 344 344
SQ SEQUENCE 344 AA; 38916 MW; 063CF2A38695BA6 CRC64;

Query Match 11.0%; Score 215.5; DB 2; Length 344;
Best Local Similarity 23.3%; Pred. No. 7.7e-05;
Matches 80; Conservative 54; Mismatches 148; Indels 61; Gaps 11;

QY 12 GTVGSALLSVQYSSTSSDRPVVWQKRDKPVTVVQSIGTEVIGTLRPD-----YRDRI 66
Db 35 GALGQDINLIPSFQMSDDDDIKWETS DK-----KKIAQFRKEKETEFEKD Y 84
QY 67 RLFEKNGSLLSLDLQADAGTYEVEISITDDTFTGKNTINLTVDPISRPQVLVASTTVLE 126
Db 85 KLFKNGTLKIKHLKHDDQDSYKVSIDYTKGNVLEKIFDLKIQERVSEPKI---SWTCIN 141
QY 127 LSEAFNLCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDDDLVSCMW 186
Db 142 T-----TLTCEVMNGTDPNLNYQDGKHLKLSQRVITHKWTTSLSAK-----FKCTA 188
QY 187 ENPISQGRSLPVKITVYRRSSLYIILS-TGGIFLLVTLTVTCACWKPSKRKOKKLEKQNS 245
Db 189 GNKVSKESSMETVSCPEKGLDIYLIIGICGGSLLMVFVALLVFIYITKRKKQRS-----242
QY 246 LEYMDQNDRLKPEADTLPRSGEQRKNPMALYILKDKSPETENPAPRPSATE-----301
Db 243 -----RRNDEELETRAH---RVATEERGRKPHQIPASTPQNPAAHQPPPPGHRSQAPSH 295
QY 302 -PGPPGYSVS-----PAVPG-----RSPGLPIRSARRYPRSP 332
```

[illegible]

RA Wilson S.D., Ulbrandt N.D., Bachy C.M., Wu H., Suzich J.A.,
RA Kiener P.A., Dall'Acqua W.F., White W.I.,
RT "Analysis of human and primate CD2 molecules by protein sequence and
RT epitope mapping with anti-human CD2 antibodies.";
RL Mol. Immunol. 41:985-1000(2004).
DR HSP; P08921; 1A64.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008424; CD2.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF05790; C2-set; 1.
FT NON TER 341
SQ SEQUENCE 341 AA; 38565 MW; DPAC90E8247194A6 CRC64;

Query Match 10.8%; Score 212.5; DB 2; Length 341;
Best Local Similarity 24.0%; Pred. No. 0.00011;
Matches 83; Conservative 56; Mismatches 140; Indels 67; Gaps 14;

QY 12 GTVGKSAALLSVQYSSTSSDRPVVWQKLRDKPVTVVQSIGTEVIGTLRP-----DYRDRI 66
Db 35 GALTQDIDLDPFQMSDDDDIKWEKTSK-----KKIAQFRKEKEFEEDAY 84
QY 67 RLFGSLLSLDLQADGTYVEISITDDTFTGKTNLTVDPIRQPVLVASTTLE 126
Db 85 KLFKNGTLKIKHLKHQDSYKVSIDTKGNVLEKTFDLKIQERVSEPKI---SWTCIN 141
QY 127 LSEAFNLNCHSHGKTSYTWLKGKPLNDSRMLSPDQKVL---ITRVLMBDDLLYS 183
Db 142 T-----TLTCEVMNGTDPFLNLYQDGK-----HVKLS--QRVITHKWTLSAK---FK 185
QY 184 CMVENPISQGRSLPKITVVRSSLYIILS--TGGIFLLVTLVTVCAWKPSKQKLEK 242
Db 186 CTAGNKVSKESRMETVSCPEGLDIYLLIGCGGSLMVFVALLVFIYTKRKQRS--- 242
QY 243 QNSLEYMDQNDRLKPEADTLPRSGEQRKNPMALYILKDKSPETENPAPEPRSAE- 301
Db 243 -----RRNDELEIRAH---RVATEERGKPHQIPASTPQNPAASQHPPPPPGHSQA 292
QY 302 ----PGPGYGSV-----PAVPG-----RPGLPPIRSARYPRSP 332
Db 293 PSHRPLPFGHRVQHQPQKRPAPSGTQVHQOGPPLPRPRVQPKPP 338

RESULT 14
Q61354 PRELIMINARY; PRT; 341 AA.
ID Q61354
AC Q61354;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Biliary glycoprotein precursor.
GN Name=Ceacam1; Synonyms=Bgph;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD1; TISSUE=Colon;
RX MEDLINE=9327328; PubMed=8500759; DOI=10.1016/0378-1119(93)90716-G;
RA McCuaig K., Rosenberg M., Turbide C., Beauchemin N., Nedellec P.;
RT "Expression of the Bgp gene and characterization of mouse colon
RT biliary glycoprotein isoforms.";
RL Gene 127:173-183(1993).
DR EMBL; X67283; CAA47700.1; -.
DR PIR; J01512; J01512.
DR HSP; Q61353; 1L6Z.
DR MGD; MGI:1347245; Ceacam1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00408; IgC2; 1.

DR PROSITE; P550835; IG_LIKE; 1.
KW Signal.
FT SIGNAL. 1 34 Potential.
SQ SEQUENCE 341 AA; 36901 MW; B5278D6606996341 CRC64;

Query Match 10.8%; Score 211; DB 2; Length 341;
Best Local Similarity 26.1%; Pred. No. 0.00014;
Matches 73; Conservative 47; Mismatches 126; Indels 34; Gaps 9;

QY 40 RDXPVTVVQSIGTEVIGTLR-----PYRDRIRLFPENGSLLLDLQADGTYVEISITD 95
Db 69 KGNPVTNAEIVHFVTGNTKTTGPAHSGRETYSNGSLLIQRTVTKDTGVYIE--MTD 126
QY 96 DTF-TGEKTNLTVDPIRQPVLVASTTLESEAFNLNCHSHGKTSYTWLKGDKPL 154
Db 127 ENFRTEATVQFHVQPVTPQSLQVNTVTKEL-DSVTITCL-SNDIGANIQLWLFNSQL 184
QY 155 LNDSRMLSPDQKVLITRVLMBDDLLYSQWENPISQGRSLPKITVVRSSLYII--- 211
Db 185 QLTERMTLSQNSILRIDPIKREDAGEYQCEISNPVSVKRSNISKLDI-----IPDPT 237
QY 212 ---LSTG-----GIFLLVTLVTVCAWKPSKQKLEKQNSLEYMDQNDRLKPEAD 261
Db 238 QGGLSDGAIAGIVGVVAGVALLAGLAYFLYSRKSQGGSDQDRLTEHKPSTSNHNLAPSD 297
QY 262 TLPRSGEQRKNPMALYILKDKSPETENPAPEPRSAE 301
Db 298 NSP-----NKVDVATVTLNFSQQPNRPTSAFSPRAE 332

RESULT 15
Q6SZ61 PRELIMINARY; PRT; 351 AA.
ID Q6SZ61
AC Q6SZ61;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cluster of differentiation 2.
GN Name=CD2;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15302161;
RA Damschroder M.M., Kozhich A.A., Woods R.M., Cheng L., Mullikin B.A.,
RA Wilson S.D., Ulbrandt N.D., Bachy C.M., Wu H., Suzich J.A.,
RA Kiener P.A., Dall'Acqua W.F., White W.I.;
RT "Analysis of human and primate CD2 molecules by protein sequence and
RT epitope mapping with anti-human CD2 antibodies.";
RL Mol. Immunol. 41:985-1000(2004).
DR EMBL; AY445036; AAR15883.1; -.
DR HSP; P08921; 1A64.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008424; CD2.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF05790; C2-set; 1.
SQ SEQUENCE 351 AA; 39580 MW; D549EA58D3CD5AE6 CRC64;

Query Match 10.7%; Score 210.5; DB 2; Length 351;
Best Local Similarity 23.5%; Pred. No. 0.00015;
Matches 84; Conservative 59; Mismatches 148; Indels 67; Gaps 14;

QY 12 GTVGKSAALLSVQYSSTSSDRPVVWQKLRDKPVTVVQSIGTEVIGTLRP-----DYRDRI 66
Db 35 GALTQDIDLDPFQMSDDDDIKWEKTSK-----KKIAQFRKEKEFEEDAY 84
QY 67 RLFGSLLSLDLQADGTYVEISITDDTFTGKTNLTVDPIRQPVLVASTTLE 126
Db 85 KLFKNGTLKIKHLKHQDSYKVSIDTKGNVLEKTFDLKIQERVSEPKI---SWTCIN 141

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 15:57:23 ; Search time 61.4446 Seconds
(without alignments)
2000.159 Million cell updates/sec

Title: US-10-706-691-20

Perfect score: 1205

Sequence: 1 MKRERGALSRSALRALAPF.....NPISQGRSLPVKITVYRRSS 240

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1201	99.7	416	2 Q8N7I3	Q8N7I3 homo sapien
2	1201	99.7	416	2 Q67IP8	Q67IP8 homo sapien
3	1192	98.9	367	2 Q6ZWL4	Q6ZWL4 homo sapien
4	1146	95.1	413	2 Q640R3	Q640R3 mus musculus
5	282	23.4	450	2 Q6UXI0	Q6UXI0 homo sapien
6	202.5	16.8	278	2 Q99232	Q99232 mus musculus
7	202.5	16.8	341	2 Q61354	Q61354 mus musculus
8	193.5	16.1	292	2 Q6UY47	Q6UY47 homo sapien
9	189.5	15.7	235	2 Q75296	Q75296 homo sapien
10	183.5	15.2	272	2 Q8RIN5	Q8RIN5 mus musculus
11	183.5	15.2	340	2 Q61349	Q61349 mus musculus
12	183.5	15.2	538	2 Q8C9E4	Q8C9E4 mus musculus
13	183.5	15.2	645	2 Q6NZB6	Q6NZB6 mus musculus
14	183.5	15.2	649	2 Q7TMP7	Q7TMP7 mus musculus
15	183.5	15.2	654	1 LV9 MOUSE	Q01965 mus musculus
16	182	15.1	471	2 Q9DAV5	Q9DAV5 mus musculus
17	181	15.0	458	2 Q61351	Q61351 mus musculus
18	181	15.0	521	2 Q61352	Q61352 mus musculus
19	178.5	14.8	475	2 Q62664	Q62664 rattus norv
20	177.5	14.7	278	2 Q61350	Q61350 mus musculus
21	177.5	14.7	341	2 Q61353	Q61353 mus musculus
22	174.5	14.5	471	2 Q9D2U0	Q9D2U0 mus musculus
23	173.5	14.4	365	2 Q6VAN5	Q6VAN5 bos taurus
24	173.5	14.4	372	2 Q6VAN6	Q6VAN6 bos taurus
25	173.5	14.4	429	2 Q6VAN7	Q6VAN7 bos taurus
26	173.5	14.4	436	2 Q6VAN8	Q6VAN8 bos taurus
27	173.5	14.4	475	2 Q810J1	Q810J1 mus musculus
28	173.5	14.4	520	2 Q925P2	Q925P2 mus musculus
29	172.5	14.3	475	2 P70161	P70161 mus musculus
30	170.5	14.1	234	2 Q78T27	Q78T27 mus musculus
31	170	14.1	300	2 Q9JHY1	Q9JHY1 rattus norv

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32 170 14.1 368 2 Q6RWT3 Q6RWT3 bos taurus
33 170 14.1 375 2 Q6RWT4 Q6RWT4 bos taurus
34 170 14.1 432 2 Q6RWT5 Q6RWT5 bos taurus
35 170 14.1 439 2 Q6RWT6 Q6RWT6 bos taurus
36 169 14.0 284 2 Q9NX42 Q9NX42 homo sapien
37 169 14.0 325 2 Q95791 Q95791 homo sapien
38 169 14.0 327 2 Q961Q7 Q961Q7 homo sapien
39 168.5 14.0 475 2 Q62056 Q62056 mus musculus
40 168 13.9 448 2 Q9JHL7 Q9JHL7 rattus norv
41 168 13.9 476 2 Q9R038 Q9R038 mus musculus
42 167.5 13.9 241 2 Q9UIB6 Q9UIB6 homo sapien
43 167.5 13.9 272 2 Q9UIB7 Q9UIB7 homo sapien
44 167.5 13.9 280 2 Q95660 Q95660 homo sapien
45 167.5 13.9 328 2 Q6FHA8 Q6FHA8 homo sapien

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ALIGNMENTS

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RESULT 1
Q8N7I3
ID Q8N7I3 PRELIMINARY; PRT; 416 AA.
AC Q8N7I3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ25530.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Tadahiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Tsugai T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
RA Nagai K., Isegai T., Sugano S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK098396; BAC05297.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 416 AA; 45994 MW; 47120CA9A00EE1CF CRC64;

Query Match 99.7%; Score 1201; DB 2; Length 416;
Best Local Similarity 99.6%; Pred. No. 1.6e-84;
Matches 239; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKRERGALSRSALRALAPFVYLLLIQTDPLEGVNTSPVRLIHGTGKSALLSVQYSST 60
Db 1 MKRERGALSRSALRALAPFVYLLLIQTDPLEGVNTSPVRLIHGTGKSALLSVQYSST 60

Qy 61 SSDRPVVKWQKRDPKVTWQSIGTEVIGTLRPDYRDRIRLFENGSLLSDLQADEGTY 120
Db 61 SSDRPVVKWQKRDPKVTWQSIGTEVIGTLRPDYRDRIRLFENGSLLSDLQADEGTY 120

Qy 121 EVELSIITDDFTFGTKTINLTVDVPIRSPQVLVASTTVLELSEAFNLNCSENGTKPSYTW 180
Db 121 EVELSIITDDFTFGTKTINLTVDVPIRSPQVLVASTTVLELSEAFNLNCSENGTKPSYTW 180

Qy 181 LKDGKPLNDSRMLLSPDQKVLITITRVLMEDDDDLYSCMVENPISQGRSLPVKITVYRRSS 240
Db 181 LKDGKPLNDSRMLLSPDQKVLITITRVLMEDDDDLYSCMVENPISQGRSLPVKITVYRRSS 240

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RESULT 2

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Q67IP8
ID Q67IP8 PRELIMINARY; PRT; 416 AA.
AC Q67IP8;

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DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Shen S., Moh M.C.;
 RT "A gene related to human hepatocellular carcinoma";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY047587; AAQ93018.1; -;
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 416 AA; 46055 MW; 7B8882298BEB4ABF CRC64;

 Query Match 99.7%; Score 1201; DB 2; Length 416;
 Best Local Similarity 99.6%; Pred. No. 1.6e-84;
 Matches 239; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MKRERGALSRSALRALAPFVYLLLIQTDPLEGVNTSPVRLIHGTGKSALLSVQYSST 60
 DB 1 MERERGALSRSALRALAPFVYLLLIQTDPLEGVNTSPVRLIHGTGKSALLSVQYSST 60

 QY 61 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRDPYDRIRLRFENGSLLSLDQLADEGTY 120
 DB 61 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRDPYDRIRLRFENGSLLSLDQLADEGTY 120

 QY 121 EVELISITDDTFTGKTNLTVDVPISRPQVLVASTTVLELSEAFNLCSHENGTKPSYTW 180
 DB 121 EVELISITDDTFTGKTNLTVDVPISRPQVLVASTTVLELSEAFNLCSHENGTKPSYTW 180

 QY 121 EVELISITDDTFTGKTNLTVDVPISRPQVLVASTTVLELSEAFNLCSHENGTKPSYTW 180
 DB 121 EVELISITDDTFTGKTNLTVDVPISRPQVLVASTTVLELSEAFNLCSHENGTKPSYTW 180

 QY 181 LKDGKPLNDSRMLLSPDKVLTITRVLMEDDDLVSCWENPISQGRSLPKITVYRRSS 240
 DB 181 LKDGKPLNDSRMLLSPDKVLTITRVLMEDDDLVSCWENPISQGRSLPKITVYRRSS 240

 RESULT 3
 Q6ZWLA PRELIMINARY; PRT; 367 AA.
 ID Q6ZWLA
 AC Q6ZWLA
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein FLJ16002.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Suzuki O., Sasaki N., Kotsuka S., Shoji T., Ichihara T., Shiohata N.,
 RA Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,
 RA Matsumura Y., Moriya S., Chiba E., Moniyama H., Onogawa S.,
 RA Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Kataoka R.,
 RA Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y.,
 RA Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T.,
 RA Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K.,
 RA Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y.,
 RA Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K.,
 RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
 RA Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK122595; BAC85486.1; -;
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KW Receptor.
 SQ SEQUENCE 367 AA; 40456 MW; 35956FA245A408F0 CRC64;

 Query Match 98.9%; Score 1192; DB 2; Length 367;
 Best Local Similarity 99.2%; Pred. No. 6.8e-84;
 Matches 238; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 QY 1 MKRERGALSRSALRALAPFVYLLLIQTDPLEGVNTSPVRLIHGTGKSALLSVQYSST 60
 DB 1 MKRERGALSRSALRALAPFVYLLLIQTDPLEGVNTSPVRLIHGTGKSALLSVQYSST 60

 QY 61 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRDPYDRIRLRFENGSLLSLDQLADEGTY 120
 DB 61 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRDPYDRIRLRFENGSLLSLDQLADEGTY 120

 QY 121 EVELISITDDTFTGKTNLTVDVPISRPQVLVASTTVLELSEAFNLCSHENGTKPSYTW 180
 DB 121 EVELISITDDTFTGKTNLTVDVPISRPQVLVASTTVLELSEAFNLCSHENGTKPSYTW 180

 QY 181 LKDGKPLNDSRMLLSPDKVLTITRVLMEDDDLVSCWENPISQGRSLPKITVYRRSS 240
 DB 181 LKDGKPLNDSRMLLSPDKVLTITRVLMEDDDLVSCWENPISQGRSLPKITVYRRSS 240

 RESULT 4
 Q64OR3 PRELIMINARY; PRT; 413 AA.
 ID Q64OR3
 AC Q64OR3
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE 290042E01Rik protein (Fragment).
 GN Name=2900042E01Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Sapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;

```

QY 74 -DKPVTVVQSGTGVIGTRDPYDRDRIRLF-ENGSLLLSDQLADSGTVEVEISIT-DDT 133
Db 62 HTMPKYLGLSNKSVVDPDL--EYQHKETMPPPNASLLINPLQFPDDEGNIVKVINQNGT 1
QY 131 FTGEXTINLTVDVPISRPOVLV-ASTTVLSELSAFTLNCNSHENGTKPSYTWLKDQKPLLN 189
Db 120 LSASQKIQTVDVDPVTRFVQVQIHPPSGAVEYVGNMILTCHVEGGTRLAYQWLKNGRPVHT 179
QY 190 DSRMLLSPDQKVLITRVLMEDDDLYSQWENPISQGRSLPVKITVY 236
Db 180 SSTYSFSPQNTLTHAPVTKEDIGNYSCLVRNPVSEMSDIIMPIIV 226

RESULT 6
Q99232 PRELIMINARY; PRT; 278 AA.
ID Q99232 AC Q99232;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Carcinoembryonic antigen family member protein precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090,
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD-1; TISSUE=Colon;
RX MEDLINE=91093141; PubMed=1985902;
RA Turbide C., Rojas M., Stanners C.P., Beauchemin N.;
RT "A mouse carcinoembryonic antigen gene family member is a calcium-
RT dependent cell adhesion molecule.";
RL J. Biol. Chem. 266:309-315(1991).
DR EMBL; X53084; CAA37251.1; -.
DR PIR; A39037; A39037.
DR PIR; JCI506; JCI506.
DR HSP; O61353; 1L6Z.
DR MGD; MGI:1347245; Ceacaml.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF000047; Ig; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Signal.
FT SIGNAL 1 34 Potential.
FT CHAIN 35 278 Potential.
SQ SEQUENCE 278 AA; 29943 MW; 1A9CEBF18770258C CRC64;

Query Match 16.8%; Score 202.5; DB 2; Length 278;
Best Local Similarity 32.1%; Pred. No. 1.3e-07;
Matches 54; Conservative 31; Mismatches 74; Indels 9; Gaps 5

QY 73 RDKPVTVVQSGTGVIGTLR----PDYDRIRLRFENGSLLLSDQLADSGTVEVEISITD 128
Db 69 KGNPVSTNAEIVHPVTGNTTKTTPGPAHSGRETYSVNGSLLIQRVTVKDGVVTIE--MTD 126

QY 129 DTF-TGEKTINLTVDVPISRPOVLVASTTVLSELSAFTLNCNSHENGTKPSYTWLKDQKPL 187
Db 127 ENFRTEATQFHQHPVTQFSLQVNTVTKEL-DSVTLTCL-SNDIGANIQLWFLNSQSL 184

QY 188 LNDSRMLLSPDKVLITRVLMEDDDLYSQWENPISQGRSLPVKITVY 235
Db 185 QLTERMTLSQNSILRDPTRKREDAGEYQCEISNPVSVRSNSIKLDI 232

RESULT 7
Q61354 PRELIMINARY; PRT; 341 AA.
ID Q61354 AC Q61354;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

```


QY 24 LLIQTDPLEGVNITSPVRLIHGTGKSALLSV-----QYSTSSDRPVVKWQ 70

$\frac{1}{2}$

RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavani T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA	Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,
RA	Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA	Jones S.J., Matra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RC	Strasbourg R.;
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR	HESBL; BC055380; AAH5380.1; -.
DR	HSSP; P08921; IHNG.
DR	GO; GO:0005615; C:extracellular space; TAS.
DR	GO; GO:0016021; C:integral to membrane; TAS.
DR	InterPro; IPR003599; IG.
DR	InterPro; IPR007110; IG-like.
DR	Pfam; PF00047; IG; 1.
DR	SMART; SM00409; IG; 2.
DR	PROSITE; PS50835; IG LIKE; 2.
FT	NON TER 1_1
SQ	SEQUENCE 649 AA; 72414 MW; AD6A093B81C063B34 CRC64;
	Query Match 15.2%; Score 183.5; DB 2; Length 649;
	Best Local Similarity 27.1%; Pred. No. 1.le-05;
	Matches 64; Conservative 45; Mismatches 108; Indels 19; Gaps 9;
QY	6 GALS---RASRALRAPFVYL-LLIQTDPLEGVNITSPVRLIHGTCKSALLSVQYSSTS 61
Db	: : : : : : : : : : : : :
	9 GPLSENPRMSQQIIFSPILIPILLFLMGLGASGETPTPTVISGMLGSTVFSLNISKDA 68
	: : : : : : : : : : : :
QY	62 SDRPVVYKWLKRDKPVTYVQSIGTEVIGTLRPPYRDRIPLFENG-SLLSDQLQADSGTY 120
Db	: : : : : : : : : : : :
	69 ETIEHI-I-WNC---PPKALALVFFVKDITILDKGYNGLRKVSDEGYSLMYNLTKSDSGSY 124
	: : : : : : : : : : : :
QY	121 EVEISITDDTFTGEKTINLTVDVIPSRPQVLVAISTTVLEL-SBAFTLNCSHENGTKPS-- 177
Db	: : : : : : : : : : : : :
	125 HAQIQNKVILTNNKEFTLHIEKLQPKIIIVSEVTPSDTDSCTFTLIC-T-VKGTKDSVQ 183
	: : : : : : : : : : : : :
QY	178 YTWLKDGKPELLNSRMLLSPDQKVLTITRVLMEDDDLYSQWENPIISQGSLPVKI 233
Db	: : : : : : : : : : : : :
	184 YSWTR-----DTHLNTYDGSHTLVASVCPCPDLPYTCKAWNPVSONSGOPVRI 233
	: : : : : : : : : : : : :

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RESULT 15
LY9 MOUSE STANDARD; PRT; 654 AA.
ID LY9
AC C01965; Q9ES29; Q9ES35; Q9ES36;
DT 01-JUN-1994 (Rel. 29, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE T-lymphocyte surface antigen Ly-9 precursor (lymphocyte antigen 9)
DE (Cell-surface molecule Ly-9).
DE Name=Ly9; Synonyms=Ly-G9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A., AND POLYMORPHISM.
RP STRAIN=129/Sv, BALB/c, and C57BL/6; TISSUE=Spleen;
RC MEDLINE=20424510; PubMed=10970093; DOI=10.1007/s002510000209;
RX Tovar V., de la Fuente M.A., Piscueta P., Bosch J., Engel P.;
RN Tovar V., de la Fuente M.A., Piscueta P., Bosch J., Engel P.;

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 15:58:02 ; Search time 22.1316 Seconds
(without alignments)
1665.085 Million cell updates/sec

Title: US-10-706-691-26

Perfect score: 1962

Sequence: 1 VNITSPVRLHGTGKSALL.....TAGVHIHQDEAGPVEISA 383

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79.*

1: Pirl.*

2: Pirl.*

3: Pirl.*

4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	218.5	11.1	351	1 RWHUC2	T-cell surface gly
2	216	11.0	341	2 JCL152	biliary glycoprote
3	207.5	10.6	278	2 JCL1506	biliary glycoprote
4	202.5	10.3	278	2 A39037	carcinoembryonic a
5	194.5	9.9	483	2 T17346	hypothetical prote
6	189	9.6	365	2 JCT780	coxsackie- and ade
7	188.5	9.6	1091	2 A58532	glial cell membran
8	188	9.6	341	2 JCL1511	biliary glycoprote
9	186.5	9.5	458	2 JCL1509	biliary glycoprote
10	185	9.4	272	2 I48268	biliary glycoprote
11	181.5	9.3	521	2 S34338	biliary glycoprote
12	180.5	9.2	347	2 S41638	T-cell surface gly
13	180.5	9.2	629	2 A46500	Ly-9.2 antigen m
14	179.5	9.1	278	2 JCL1507	biliary glycoprote
15	176.5	9.0	475	2 A54879	pregnancy-specific
16	173.5	8.8	344	1 RWRTC2	T-cell surface gly
17	173.5	8.8	353	1 IJUBNC	neural cell adhesi
18	172.5	8.8	858	1 IJRTWC	neural cell adhesi
19	170.5	8.7	526	1 A32184	biliary glycoprote
20	170.5	8.7	1227	2 T23004	hypothetical prote
21	168	8.6	761	1 IJUHNG	neural cell adhesi
22	166	8.5	458	2 S68177	C-CAM2a protein is
23	166	8.5	458	2 S23969	ecto-ATPase precu
24	166	8.5	519	2 A44783	neural cell adhesi
25	166	8.5	1091	1 IJCHNL	pregnancy-specific
26	165	8.4	475	2 I76668	functional adhesio
27	164.5	8.4	299	2 S56749	transmembrane carc
28	164	8.4	464	2 C30127	neural cell adhesi
29	163.5	8.3	725	2 JB0100	

30	162	8.3	1115	1 IJMSNL	neural cell adhesi
31	161.5	8.2	458	1 WMSR1	biliary glycoprote
32	161.5	8.2	521	2 JCL1508	biliary glycoprote
33	161.5	8.2	1092	1 JN0635	neural cell adhesi
34	161	8.2	1232	2 T43027	neural cell adhesi
35	159.5	8.1	725	1 IJMSNG	neural cell adhesi
36	159	8.1	344	2 A27681	nonspecific cross-
37	158.5	8.1	709	2 A35364	carcinoembryonic a
38	157	8.0	324	2 G43354	pregnancy-specific
39	157	8.0	326	2 F43354	pregnancy-specific
40	157	8.0	333	2 A43354	pregnancy-specific
41	157	8.0	335	2 H43354	pregnancy-specific
42	156.5	8.0	406	2 E43354	pregnancy-specific
43	156.5	8.0	428	2 A27658	pregnancy-specific
44	156	8.0	344	2 B28967	T-cell surface gly
45	155.5	7.9	419	2 B54312	pregnancy-specific

ALIGNMENTS

RESULT 1

RWHUC2

T-cell surface glycoprotein CD2 precursor - human

N;Alternate names: E rosette receptor; erythrocyte receptor; erythrocyte-binding protein

C;Species: Homo sapiens (man)

C;Date: 31-Mar-1989 #sequence revision 31-Mar-1989 #text change 09-Jul-2004

C;Accession: A28967; A26486; B26486; A28416; A28023; S02292; A30430; S00829; A29874

R;Diamond, D.J.; Clayton, L.K.; Sayre, P.H.; Reinherz, E.L.

A;Title: Exon-intron organization and sequence comparison of human and murine T11 (CD2)

A;Reference number: A28967; MUID:88144486; PMID:2894031

A;Accession: A28967

A;Molecule type: DNA

A;Residues: 1-351 <DIA>

A;Cross-references: UNIPROT:P06729; GB:M19806; GB:J03622; GB:J03623; NID:G180079; PIDN:AJ

R;Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.

Proc. Natl. Acad. Sci. U.S.A. 83, 8718-8722, 1986

A;Title: Molecular cloning of the human T-lymphocyte surface CD2 (T11) antigen.

A;Reference number: A26486; MUID:87041523; PMID:3490670

A;Accession: A26486

A;Molecule type: mRNA

A;Residues: 1-338,'M',340,'Q'QKTHCPLPLIKKDRNCLFQ' <SE1>

A;Accession: B26486

A;Molecule type: protein

A;Residues: 25-46,'X',50 <SE2>

R;Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.

Proc. Natl. Acad. Sci. U.S.A. 84, 7256, 1987

A;Reference number: A28416

A;Contents: revision

A;Accession: A28416

A;Molecule type: mRNA

A;Residues: 333-351 <SE3>

R;Seed, B.; Aruffo, A.

Proc. Natl. Acad. Sci. U.S.A. 84, 3365-3369, 1987

A;Title: Molecular cloning of the CD2 antigen, the T-cell erythrocyte receptor, by a rapid

A;Reference number: A28023; MUID:87204137; PMID:2437578

A;Accession: A28023

A;Molecule type: mRNA

A;Residues: 1-265,'Q',267-351 <SEE>

A;Cross-references: GB:M16445; NID:G178668; PIDN:AAA51738.1; PID:G178669

R;Sayre, P.H.; Chang, H.C.; Hussey, R.E.; Brown, N.R.; Richardson, N.E.; Spagnoli, G.; C

Proc. Natl. Acad. Sci. U.S.A. 84, 2941-2945, 1987

A;Title: Molecular cloning and expression of T11 cDNAs reveal a receptor-like structure

A;Reference number: S02292; MUID:87204243; PMID:2893656

A;Accession: S02292

A;Molecule type: mRNA

A;Residues: 1-338,'M',340,'Q'QKTHCPLPLIKKDRNCLFQ' <SA1>

A;Cross-references: GB:M16336; NID:G180093; PIDN:AAA51946.1; PID:G180094

A;Accession: A30430

A;Molecule type: protein

A;Residues: 25-43,152-163 <SA2>

R;Lang, G.; Wotton, D.; Owen, M.J.; Sewell, W.A.; Brown, M.H.; Mason, D.Y.; Crumpton, M.

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F;87,104,153,195/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          11.0%; Score 216; DB 2; Length 341;
Best Local Similarity 26.1%; Pred. No. 2.9e-06;
Matches              73; Conservative 48; Mismatches 125; Indels 34; Gaps 9;

Qy      40 RDKPVTVVQSIGTEVIGTLR-----PDYRDRIRLFENGSLLLSDQLADEGTYEVEISITD 95
       :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      69 KGNPVSTNAIEIVHQVGTGNTKTTTTPGAHSGRETIVYSNGSLLIQRVTWKDTGVYTIE--MTD 126

Qy      96 DTF-TGEKTINLTVDVPISRPQVLVASTTVLELSEAF TLNCSHENGTKPSYTWLKDGKPL 154
       :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      127 ENFRRT EATVQH FHVHPQTQPSLQVNTTVTKEL-DSVTLTCL-SNDIGANIQLWFLNSQSL 184

Qy      155 LNDSRMLLSDPQKVLTITRVLMEDDDDLYSWCWENPISQGRSLPKVITVRRSSLYII--- 211
       ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      185 QLTERMTLSQNNSILRIDPIKREDAGEYOCEISNPVSVKRSNIKLDI-----IFDPT 237

Qy      212 ----LSTG-----GIPLLTVTCACWKPSKKQKLEKQNSLEYMDQNDRLKP EAD 261
       ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      238 QGGLSDCATAGIVIGVVAGVALLAGLAYFLYSRKSGGSDQRDLTEHKPSTSHNNLAPSD 297

Qy      262 TLP RSQEQRKNPMALYILKDKDSPETEENPAPEPRSAT 301
       :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      298 NSP-----NKVDDVAVTVLNFNSQQPNRPTSAPPSPRATE 332


RESULT 3
JC1506
biliary glycoprotein B - mouse
C/Species: Mus musculus (house mouse)
C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C/Accession: JC1506
R/McCuigaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
A/Title: Expression of the Bgp gene and characterization of mouse colon biliary
A/Reference number: JC1505; PMID:93273228; PMID:8500759
A/Accession: JC1506
A>Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-278 <MCC>
A/Cross-references: UNIPROT:Q99232
C/Comment: This protein is expressed at the cell surface and plays a determinant
C/Genetics:
A/Gene: Bgpb
C/Superfamily: biliary glycoprotein; carcinoembryonic antigen precursor amino-t-
C/Keywords: glycoprotein; receptor
F/I-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA>
F/I59-216/Domain: immunoglobulin homology <IMM>
F;87,104,153,195/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          10.6%; Score 207.5; DB 2; Length 278;
Best Local Similarity 32.1%; Pred. No. 7.5e-06;
Matches              54; Conservative 32; Mismatches 73; Indels 9; Gaps 5;

Qy      40 RDKPVTVVQSIGTEVIGTLR-----PDYRDRIRLFENGSLLLSDQLADEGTYEVEISITD 95
       :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      69 KGNPVSTNAIEIVHQVGTGNTKTTTTPGAHSGRETIVYSNGSLLIQRVTWKDTGVYTIE--MTD 126

Qy      96 DTF-TGEKTINLTVDVPISRPQVLVASTTVLELSEAF TLNCSHENGTKPSYTWLKDGKPL 154
       :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      127 ENFRRT EATVQH FHVHPQTQPSLQVNTTVTKEL-DSVTLTCL-SNDIGANIQLWFLNSQSL 184

Qy      155 LNDSRMLLSDPQKVLTITRVLMEDDDDLYSWCWENPISQGRSLPKVITV 202
       :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      185 QLTERMTLSQNNSILRIDPIKREDAGEYOCEISNPVSVKRSNIKLDI 232


RESULT 4
A39037
carcinoembryonic antigen mcmGM2 precursor - mouse
N/Alternate names: biliary glycoprotein homolog; calcium-dependent cell adhesio
C/Species: Mus musculus (house mouse)
```

[illegible]

Query Match	9.6%;	Score 189;	DB 2;	Length 365;	
Best local Similarity	23.2%;	Pred. No. 0.00015;			
Matches	91;	Conservative 63;	Mismatches 137;	Indels 102;	Gaps 19
Qy	1	WNITSPVRLIHGTGKSGALLSVQYSSTSSDR-pv-vkwolkrdkpvvtvqvgi----	grev	54	
Db	20	LSITTPQMIETAKAGETAYLPCKETLPGEDQGLDIEWLLSPADNKQDVQVILVSGDKI	79		
Qy	55	IGTLRPDYRDIRLFEN-----GSLLSLDQLADEGTYVEIISITDDTFTGKKTINITV	108		
Db	80	YDDYVYQDLKGRVHTSNDLKSGDASINVTNLQISDIGTYQCKVKKAPG--VGNKKIQLTV	137		
Qy	109	DVPIRSRQVILVASTVITLSEAFPLNCSHENGTKP-SYTWLKGKGLPLNDSRML-	161		
Db	138	LVKPSGIRCYVDGSE--EIGNDFKFKCEKPGSLPLRYEOK-----LSDSQKLPTSNLP	190		
Qy	162	--LSPDKQVLTITRVLMEDDLSCWVENPISQGRSLPVKITVYRRSS-----LVIIILST	214		
Db	191	EMTSP--VISVKNASAEYSTGYTCTVNRNVGSDQCL-LRLDVPVPSNRAGTIAGAVIGT	246		
Qy	215	GGIFLLVTLVTVCACWKPFRKQKKLEKQNSLEWMDQNDRLKPEADTLPRSGEGRKNP	274		
Db	247	LLALVLIALIVFC-CHK--KRREKYEKE-----VHHDIR-----	278		
Qy	275	MALYILKDKDSPETEENPAPRPSATEP---GPPGYSVPSPVPGKSPG-----LPRI	323		
Db	279	-----EDVPPKSRSTARSYIGNSHSLGMSPSNMEGYSKTYQNVQFSE	324		
Qy	324	SARRYPRSPARSPATGTHSSPPRAPSPQRSR	356		
Db	325	DLBRAPQSP-----TLPPAKVAAPNLRS	347		

RESULT 7
A58532
glial cell membrane glycoprotein LIG-1 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text
C:Accession: A58532
R:Suzuki, Y.; Sato, N.; Tohyama, M.; Wanaka, A.; Takagi,
R.

J. Biol. Chem. 271, 22522-22527, 1996
A;Title: cDNA cloning of a novel membrane glycoprotein that is expressed specifically in
A;Reference number: A58532; MUID:96394313; PMID:8798419
A;Accession: A58532
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1091 <SUZ>
A;Cross-references: UNIPROT:P70193; GB:D78572; NID:G1545806; PIDN:BAAL1416.1; PID:G15458
F;36-61/Domain: proteoglycan amino-terminal homology <PAH>
F;71-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;95-117/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;118-141/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;142-165/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;166-189/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;191-213/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;214-237/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;238-261/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;262-285/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;286-309/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
F;310-333/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
F;334-357/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
F;358-381/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
F;385-408/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
F;409-432/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
F;440-485/Domain: proteoglycan carboxyl-terminal homology <PCH>

Query Match 9.6%; Score 188.5; DB 2; Length 1091;
Best Local Similarity 21.1%; Pred. No. 0.0006;
Matches 79; Conservative 56; Mismatches 122; Indels 117; Gaps 16;

Qy 12 GTVCKSALLSVQYSTSSDRPVKWKLRDKPVTTVQSIGTEVIGTLRPDYRIRLF-- 69
Db 615 GTTAR-----DECAATHNPQIAWQ--KQG-----GTFPPAARER-RMHVM 653

Qy 70 -ENGLLSLDQLADEGTYEVEISITDFTTGEKTIINLTVDVIPSRQVLV-ASTTVLEL 127
Db 654 PDDVFFITVDKIDMGVY-----SCTAQSAGSVSANATLV-LETSLAVPLEDRVTV 708

Qy 128 SEATFLNCSHENGKYPSTWTKGKPLNDSRMLSPDQKVLTTTRVLMEDDDLYSCWVE 187
Db 709 GETVAFOCKATGSPTRITWTKGGRPLSLTERHFTFGNQLLVVQNMIDDAGRYTCMS 768

Qy 188 NPISQGRSLPVKITVYRRSSLYIILSTG-----GIF-----LLVTLVTVCACWK 231
Db 769 NPLGTERA-----HSQSLIPTGCRKDGTTVGIFTAVCSVLISLWVWCIIYQ 819

Qy 232 PSKRKQK-----KLEKQNSLE-----YMDQN----- 252
Db 820 TRKKSEEVNTDETIVPPDPVPSVLSQGLSDRQETVVRTEGGHQANGHIESNGVCLR 879

Qy 253 DDLKPEADTLPRGQER-----KNPMALYILKDKD-----SPETE 289
Db 880 DPSLPFPEVDIHSITCRQPKLGVGTREPKVTEKADRTAAPHTTAHSGSVCDCSTDTA 939

Qy 290 ENPAPERASATRG 303
Db 940 YHPQFVPRDSGQPG 953

RESULT 8
JC1509
biliary glycoprotein G - mouse
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: JC1511
R;McCuagig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
A;Title: Expression of the Bgp gene and characterization of mouse biliary glycopro
A;Reference number: JC1505; MUID:93273228; PMID:8500759
A;Accession: JC1511
A;Molecule type: DNA
A;Residues: 1-341 <MCC>
A;Cross-references: UNIPROT:Q61353; GB:X67282

C;Comment: This protein is expressed at the cell surface and plays a determinant role in
C;Genetics:
A;Gene: Bgpg
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: glycoprotein; receptor
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;75-124/Domain: immunoglobulin homology <IMM1>
F;159-216/Domain: immunoglobulin homology <IMM2>
F;71,89,104,153,195/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;71,89,104,153,195/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.6%; Score 188; DB 2; Length 341;
Best Local Similarity 25.2%; Pred. No. 0.00015;
Matches 64; Conservative 45; Mismatches 115; Indels 30; Gaps 8;

Qy 62 YRDIRLRFENGSLLSLDQLADEGTYEVEISITDFTTGEKTIINLTVDVIPSRQVLVA 120
Db 95 YSGREIYNSGSLFQMITMKDMGVYTLD--MTDENYRRTQATVRFHVHPVTPQPFLOVT 152

Qy 121 STTVLELSEAFTLNCSHENGKTPSTWTKGKPLNDSRMLSPDQKVLTTTRVLMEDDD 180
Db 153 NTTVKEL-DSVTITCL-SNDIGANIQWLFNFSQSLQTLTERMTLSQNSILRIDPIKREDAG 210

Qy 181 LYSCHWENPISQGRSLPVKITVYRRSSLYI-----LSTG-----GIFLLVTLVTVC 227
Db 211 EYQCEISNPVSVRRSNSIKLDI-----IFDPTQGGSLSDGAIAGIVGVVAGVALLIAGL 263

Qy 228 ACKPKRKKQKLEKQNSLEYMDNDRLKPEADTLPRSGEQERKNPMALYILKDKDSPE 287
Db 264 AYLKSRKSGGSDQRDLTEHKPSTNHNILAPSDNGP-----NKVDDVAYTVTLNFSQQP 318

Qy 288 TEENPAPEPRSAT 301
Db 319 NRTSAPSSPRATE 332

RESULT 9
JC1509
biliary glycoprotein E - mouse
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: JC1509
R;McCuagig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
A;Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopro
A;Reference number: JC1505; MUID:93273228; PMID:8500759
A;Accession: JC1509
A;Molecule type: mRNA
A;Residues: 1-458 <MCC>
A;Cross-references: UNIPROT:Q61351; GB:X67280
C;Comment: This protein is expressed at the cell surface and plays a determinant role in
C;Genetics:
A;Gene: Bgpe
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: glycoprotein; receptor
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;160-219/Domain: immunoglobulin homology <IMM1>
F;254-303/Domain: immunoglobulin homology <IMM2>
F;339-396/Domain: immunoglobulin homology <IMM3>
F;87,104,148,199,206,210,226,258,290,294,304,333,375/Binding site: carbohydrate (Asn) (c

Query Match 9.5%; Score 186.5; DB 2; Length 458;
Best Local Similarity 27.4%; Pred. No. 0.00027;
Matches 52; Conservative 38; Mismatches 83; Indels 17; Gaps 6;

Qy 40 RDKPVTVQSIGTEVIGTLR----PDYRDIRLRFENGSLLSLDQLADEGTYEVEISITD 95
Db 69 KGNPVSNAEIVHQVTGNTTKTTGPAHSGRETVYNSGSLTIQRVTVKDGTVTYIE--MTD 126

Qy 96 DTF-TGEKTIINLTVDVIPSRQVLVASTTVLELSEAFETLNC-SHENGKTPSYTWLKDQKP 153
Db 127 ENFRTEATQVQFVHPVLLKPNITSNNSNVEGSDSVSLTCDSTDPDNITILNRSNGES 186

Qy 154 LLNDSRMLSPDQKVLTTTRVLMEDDDLYSCWENPISQGRSLPVKITVYRRSSLYI----- 209

Db 187 LSEGRDLKSLSEGNRLTLNLTNRDTPGYVCETRNPNVNSRDPFSLNI-----IYGPDT 241
QY 210 IILSTGGIFL 219
Db 242 PIISPSDIYL 251

RESULT 10
148268
biliary glycoprotein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48268
R:Nedellec, P.; Dveksler, G.S.; Daniela, E.; Turbide, C.; Chow, B.; Basile, A.A.; Holmes, J. Virol. 68, 4525-4537, 1994
A:Title: Bgp2, a new member of the carcinoembryonic antigen-related gene family, encodes A:Reference number: A53995; MUID:94267915; PMID:8207827
A:Accession: I48268
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-272 <RES>
A:Cross-references: UNIPROT:Q8R1N5; EMBL:X76085; NID:G511020; PIDN:CAA53699.1; PID:G5110
C:Genetics:
A:Gene: Bgp2
C:Superfamily: biliary glycoprotein; carcinoembryonic antigen precursor amino-terminal h
C:Keywords: glycoprotein
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F:159-216/Domain: immunoglobulin homology <IMW>

Query Match 9.4%; Score 185; DB 2; Length 272;
Best Local Similarity 25.7%; Pred. No. 0.00018;
Matches 62; Conservative 45; Mismatches 86; Indels 48; Gaps 9;

QY 10 IHGTGKSAALSV-----QVSTSSDRPVVWQKDKPVTVVQSIGTEVIG 56
Db 43 LHAAGNNVILVWYNNMKGVSAFHWKGGSTTNAEIVRFVTGNTKTIK----- 91

QY 57 TLRDPRDRIRLFENGSLLSLDQLADRGTEVEISITDDTF-----TGEKTNLTVDVP 111
Db 92 --GPVHSGRETLVNGSLLIQRTVMKDTGVVTIE--MTDQNYRRRLVTGQ----FHVHQP 143

QY 112 ISRPQVLVASTVLELSEAFNLNCSHENGTPKPSVTWLDKGLPLNDSRMLLSPDQKVITI 171
Db 144 VTQPSLQVNTVTKEL-DSVTLTCLSKD-ROAHIHIFNNDTLITKQWTSQAGLILKI 201

QY 172 TRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSSLYI-----ILSTG---GIFLLVT 222
Db 202 DPIKREDAGEYQCEISNPVSKRSNSIKLEIVFDSTVDISDVPIAVIITGAVAGVILIAG 261

QY 223 L 223
Db 262 L 262

RESULT 11
S34338
biliary glycoprotein F - mouse
N:Alternate names: mouse hepatitis virus (MHV) receptor glycoprotein
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S34338; JCL1510; A41093
R:Huang, D.C.; Huang, X.F.; Novel, M.; Novel, G.
submitted to the EMBL Data Library, July 1992
A:Description: A Clp-family gene present on the lactose-protease plasmid of lactococcus
A:Reference number: S34338
A:Accession: S34338
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-521 <HUA>
A:Cross-references: UNIPROT:Q61352; EMBL:X67281; NID:G312585; PIDN:CAA47698.1; PID:G3125
R:McQuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993

A:Title: Expression of the Bgp gene and characterization of mouse colon biliary glycoprotein
A:Reference number: JCL1505; MUID:93273228; PMID:8500759
A:Accession: JCL1510
A:Molecule type: mRNA
A:Residues: 1-81,'Q',83-141,'P',143-521 <MCC>
A:Cross-references: GB:X67281
R:Williams, R.K.; Jiang, G.S.; Holmes, K.V.
Proc. Natl. Acad. Sci. U.S.A. 88, 5533-5536, 1991
A:Title: Receptor for mouse hepatitis virus is a member of the carcinoembryonic antigen
A:Reference number: A41093; MUID:91288498; PMID:1648219
A:Accession: A41093
A:Status: preliminary
A:Molecule type: protein
A:Residues: 35-59 <WL>
C:Comment: This protein is expressed at the cell surface and plays a determinant role in
C:Genetics:
A:Gene: Bgpf
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C:Keywords: glycoprotein; receptor
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F:160-219/Domain: immunoglobulin homology <IMM1>
F:254-303/Domain: immunoglobulin homology <IMM2>
F:339-396/Domain: immunoglobulin homology <IMM3>
F:87,104,148,199,206,210,226,258,290,294,304,333,375/Binding site: carbohydrate (Asn) (C
F:87,104,148,199,206,210,226,258,290,294,304,333,375/Binding site: carbohydrate (Asn) (C

Query Match 9.3%; Score 181.5; DB 2; Length 521;
Best Local Similarity 27.4%; Pred. No. 0.00065;
Matches 52; Conservative 37; Mismatches 84; Indels 17; Gaps 6;

QY 40 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLSLDQLADRGTEVEISITD 95
Db 69 KGNPVSNTAEIVHPVTGNTKTTGPAHSGRETVVYNGSLLIQRTVMKDTGVVTIE--MTD 126

QY 96 DTP-TGEKTNLTVDVPISRPQVLVASTVLELSEAFNLNCSHENGTPKPSVTWLDKGP 153
Db 127 ENFRTEATQFHVHQLLKPNTNNSNPNVEGDSVSLTCDSTDPDNTITVLSRNGES 186

QY 154 LLNDSRMLLSPDQKVITITRVLMEDDLYSCMVENPISQGRSLPVKITVYRRSSLYI--- 209
Db 187 LSEGRDLKSLSEGNRLTLNLTNRDTPGYVCETRNPNVNSRDPFSLNI-----IYGPDT 241

QY 210 IILSTGGIFL 219
Db 242 PIISPSDIYL 251

RESULT 12
S41638
T-cell surface glycoprotein CD2 precursor - horse
N:Alternate names: T-lymphocyte surface antigen CD2
C:Species: Equus caballus (domestic horse)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S41638; S31578
R:Tavernor, A.S.; Kydd, J.H.; Bodian, D.L.; Jones, E.Y.; Stuart, D.I.; Davis, S.J.; Butcl
Eur. J. Biochem. 219, 969-976, 1994
A:Title: Expression cloning of an equine T-lymphocyte glycoprotein CD2 cDNA. Structure-b
A:Reference number: S41638; MUID:94155904; PMID:7906650
A:Accession: S41638
A:Molecule type: mRNA
A:Residues: 1-347 <TAV>
A:Cross-references: UNIPROT:P37998; EMBL:X69884; NID:G1057; PIDN:CAA49511.1; PID:G1058
C:Superfamily: T-cell surface glycoprotein CD2
C:Keywords: glycoprotein; surface antigen; T-cell; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-347/Product: T-cell surface glycoprotein CD2 #status predicted <MAT>

Query Match 9.2%; Score 180.5; DB 2; Length 347;
Best Local Similarity 26.8%; Pred. No. 0.00046;
Matches 80; Conservative 42; Mismatches 121; Indels 55; Gaps 14;

QY 68 LFENGSLLSLDQLADRGTEVEISITDDTFTEKTNLTVDVPISRPQVLVASTVLEL 127
Db 81 VLKNGTLKIKHLRIHEGTYKVDAYSDDGKNVLEETPHLSLLEWVSKPNISWSCTNT--- 137

```
QY 128 SEAFILNCSEHGKPSYTWLKGKPLLNDSRMLSPDQKVLITITRVLMEDDDLVSCWVE 187
Db 138 -----TLTCEVTGKDFE---LK-----LYLNGRMILQKSPKVIIVYKRASNQIAS-FKCTAN 185
QY 188 NPISQGRSLPKVITVYRRSSLIYI--LSTGGIFLLVTLVTVACAWKPSKQKQKLEKQNS 245
Db 186 NTVSEESSVVIRCTEGLDILYISGICGGIILFVFLALL--IFYISKKK-----KQNS 238
QY 246 LEYNDQNDRLKPADTLPRSGEGEGRKNPMALYILKDKSPETEENPA-----PSPRSATEP 302
Db 239 ----RRNDEELEIRAHKV--ISEERGRKPHQI-----PGSTPLNPAASQPPPPSHRP 285
QY 303 GPQCYSVSPVPGSRGSLP-IRSARRYPRSPARSPAT-----GRTHSSPPR 347
Db 286 QAPGH--RPQVPGHRPLPPGHRVHOQOQKRAPPTPGTQAHQOQKGPPLPRPRVQPKPR 341

RESULT 13
A46500
Ly-9.2 antigen - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A46500
R:Sandrin, M.S.; Gumley, T.P.; Henning, M.M.; Vaughan, H.A.; Gonez, L.J.; Trapani, J.A.;
J. Immunol. 149, 1636-1641, 1992
A:Title: Isolation and characterization of cDNA clones for mouse Ly-9.
A:Reference number: A46500; MUID:92373005; PMID:1506686
A>Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-629 <SAN>
A:Cross-references: GB:M84412; NID:g198931; PIDN:AAA39468.1; PID:g198932
A:Experimental source: C57BL/6
A:Note: sequence extracted from NCBI backbone (NCBIN:111651, NCBIPI:111654)
C:Keywords: transmembrane protein

Query Match 9.2%; Score 180.5; DB 2; Length 629;
Best Local Similarity 27.5%; Pred. No. 0.00095;
Matches 55; Conservative 40; Mismatches 90; Indels 15; Gaps 7;

QY 5 SPVRLIHGTGKSAALLSVQYSTSSDRPVVWQKLRDKPVTTVVQSIGTEVIGTLRPDYRD 64
Db 29 TPPTVISGLGSGVTFSNLISKDAEIHII-WNC---PPKALALVFFYKKDITILDKYNG 84
QY 65 RIRLPENG-SLLLSDLQADGTEVEISITDDFTGKTLNLTVDVPISRPQVLVASTT 123
Db 85 RLKVSDEGSLYMGSLNLTGSDSGYHAQINQKNVILTTNKEFTLHIYEKLOKQPIIVESVT 144
QY 124 VLEL-SEAFILNCSEHGKTPS--YTWLKGKPLLNDSRMLSPDQKVLITITRVLMEDDDD 180
Db 145 PSDTDSCTFTLICT-VKGTQDSVQSWTRE-----DTHLNTYDGSHTLRVSQVCDPDL 197
QY 181 LYSQWENPISQGRSLPKVI 200
Db 198 PYTCANPNVQNSQSPVRI 217

RESULT 14
JCI507
biliary glycoprotein C - mouse
C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C:Accession: JCI507
R:McCuaign, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
A:Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopro
A:Reference number: JCI505; MUID:93273228; PMID:8500759
A:Accession: JCI507
A:Molecule type: mRNA
A:Residues: 1-278 <MCC>
A:Cross-references: UNIPROT:Q61350; GB:X67278
C:Comment: This protein is expressed at the cell surface and plays a determinant role in
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C:Genetics:

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A:Gene: BpPC
C:Superfamily: biliary glycoprotein; carcinoembryonic antigen precursor amino-terminal h
C:Keywords: glycoprotein; receptor
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;75-124/Domain: immunoglobulin homology <IMM1>
F;159-216/Domain: immunoglobulin homology <IMM2>
F;71,89,104,153,195/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.1%; Score 179.5; DB 2; Length 278;
Best Local Similarity 31.7%; Pred. No. 0.0004;
Matches 45; Conservative 29; Mismatches 63; Indels 5; Gaps 4;

QY 62 YRDRIELFENGSLLLSDQLADGTYEVEISITDDFTGKTLNLTVDVPISRPQVLVA 120
Db 95 YSGREIYINGSLLFQMITWKMGGVTLDB--WDENYRRTQATVRFVHQVTPQFLQVT 152
QY 121 STTVLSEAFILNCSEHGKTPSYTWLKGKPLLNDSRMLSPDQKVLITITRVLMEDDDD 180
Db 153 NTTVKEL-DSVTLTCL-SNDIGANIQLFNSQSLQTLTERMTLSQNNISILRIDPIKREDAG 210
QY 181 LYSQWENPISQGRSLPKVITV 202
Db 211 EYQCEISNPNVSRRSNIIKLDI 232

RESULT 15
A54879
pregnancy-specific glycoprotein rncgm3 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C:Accession: A54879
R:Chen, H.; Chen, C.L.; Chou, J.Y.
Biochemistry 33, 9615-9626, 1994
A:Title: Characterization of two promoters of a rat pregnancy-specific glycoprotein gene
A:Reference number: A54879; MUID:94347731; PMID:8068638
A:Accession: A54879
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-475 <CHE>
A:Cross-references: UNIPROT:Q62664; GB:U09815; NID:g497254; PIDN:AAA56870.1; PID:g497255
A:Note: authors translated the codon GCT for residue 64 as Gly
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termina
C:Keywords: glycoprotein
F;1-137/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA1>
F;242-378/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA2>
F;399-456/Domain: immunoglobulin homology <IMM2>
```

```
Query Match 9.0%; Score 176.5; DB 2; Length 475;
Best Local Similarity 32.3%; Pred. No. 0.0012;
Matches 64; Conservative 24; Mismatches 95; Indels 15; Gaps 8;

QY 11 HGTVGKSAALLSVQYSTSSDRPVVKW-----QLKRDKPVTVVQSIGTEVIGTLRPDYRDR 65
Db 284 HAVEGESVLLYVH--NLPEALQTFWSYKGYSLKEPK--IAEYSIATKSVFP-GPAHRGR 338
QY 66 IRLFENGSLLLSDQLADGTYEVEISITDDFTGKTLNLTVDVPISRPQVLVASTTV- 124
Db 339 ATGTYGSLLLQDLTARDTGLTYL-VILDSNISKAPQVQVTHKPTQFLRTESTVT 397
QY 125 LELSEAFILNCSEHGKTPSYTWLKGKPLLNDSRMLSPDQKVLITITRVLMEDDDDLYSC 184
Db 398 VQSSVWFT--CLSDN-TGVSIRMLFKQNQLQVTERMTLSPSNCQLRIHDVRRREDAGQYRC 454
QY 185 MVENPISQGRSLPKVITV 202
Db 455 EAFNPISKTSRSPVSLAV 472
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Search completed: July 26, 2005, 16:14:17
Job time : 23.1316 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 15:58:52 ; Search time 28.2793 seconds
(without alignments)
1011.008 Million cell updates/sec

Title: US-10-706-691-26

Perfect score: 1962

Sequence: 1 VNITSPVRLHGTGKSALL.....TAGVHIHQDEAGPVEISA 383

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:**

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp:**
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp:**
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp:**
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp:**
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp:**
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	268	13.7	450	4	US-09-907-794A-320
2	268	13.7	450	4	US-09-905-125A-320
3	268	13.7	450	4	US-09-902-775A-320
4	268	13.7	450	4	US-09-906-700-320
5	268	13.7	450	4	US-09-903-603A-320
6	268	13.7	450	4	US-09-904-920A-320
7	268	13.7	450	4	US-09-909-064-320
8	268	13.7	450	4	US-09-905-381A-320
9	268	13.7	450	4	US-09-906-618-320
10	218.5	11.1	351	3	US-08-466-465-6
11	218.5	11.1	351	4	US-08-730-465-6
12	199.5	10.2	1101	3	US-08-986-485-2
13	196.5	10.0	387	3	US-08-175-928-2
14	195	9.9	316	4	US-08-397-243D-13
15	189.5	9.7	319	1	US-08-597-495B-22
16	189.5	9.7	319	3	US-08-068-051A-22
17	189.5	9.7	319	4	US-09-336-536-67
18	189.5	9.7	319	4	US-08-234-465A-6
19	189.5	9.7	319	4	US-09-953-499-6
20	188.5	9.6	1091	3	US-08-986-485-5
21	185	9.4	365	2	US-08-979-424-3
22	185	9.4	365	3	US-08-928-383B-2
23	185	9.4	365	3	US-09-272-496-2
24	185	9.4	365	4	US-09-949-016-6064
25	185	9.4	383	4	US-09-949-016-11050
26	184	9.4	365	3	US-08-928-383B-26
27	183.5	9.4	270	4	US-09-254-465A-24

Sequence 24, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 6, Appl
Sequence 24, Appl
Sequence 6428, Ap
Sequence 483, App
Sequence 7327, Ap
Sequence 4, Appl
Sequence 24, Appl
Sequence 10, Appl
Sequence 12, Appl
Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-09-907-794A-320
; Sequence 320, Application US/09907794A

; Patent No. 6635468

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCES: 10466-14

; CURRENT APPLICATION NUMBER: US/09/907,794A

; PRIOR FILING DATE: 2001-07-17

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547

APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 320
LENGTH: 450
TYPE: PRT
ORGANISM: Homo Sapien
US-09-907-794A-320

Query Match 13.7%; Score 268; DB 4; Length 450;
Best Local Similarity 31.9%; Pred. No. 1.4e-13;
Matches 67; Conservative 43; Mismatches 90; Indels 10; Gaps 7;
Qy 1 VNITSPVRLIHGTGKSGALLSVQYS--STSSDRPVKWKQLKR--DKPVTVVQSIGTEVIG 56
Db 20 LKVTVPSTHVGVRGQALYLPVHYGFHTPASDIQII-WLPERHTMPKYLGSVKNKSWP 78
Qy 57 TLRPDYDRIRLF-ENGSLLSLDLQADGTYEVEISIT-DDTFTGKTNLTVDVPIR 114
Db 79 DL--EYQHKFTMPNPASLLINPLQFPDEGNYIVKVNIGQNGTSLASQKIQTVDVDPVK 136
Qy 115 PQVLV-ASTTVLELSEAFITLNCSENGTKPSYTWLKGKPLNDSRMLLSPDQKVLITR 173
Db 137 PVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSTYSFSPQNTLTIAP 196
Qy 174 VLMEDDDLVSCMVENPISQGRSLPVKITVY 203
Db 197 VTKEIDIGNYCLVRNPVSEMSDIIMPIIY 226

RESULT 2
US-09-905-125A-320
Sequence 320, Application US/09905125A
Patent No. 6664376
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann

Query Match 13.7%; Score 268; DB 4; Length 450;
Best Local Similarity 31.9%; Pred. No. 1.4e-13;
Matches 67; Conservative 43; Mismatches 90; Indels 10; Gaps 7;
Qy 1 VNITSPVRLIHGTGKSGALLSVQYS--STSSDRPVKWKQLKR--DKPVTVVQSIGTEVIG 56
Db 20 LKVTVPSTHVGVRGQALYLPVHYGFHTPASDIQII-WLPERHTMPKYLGSVKNKSWP 78
Qy 57 TLRPDYDRIRLF-ENGSLLSLDLQADGTYEVEISIT-DDTFTGKTNLTVDVPIR 114
Db 79 DL--EYQHKFTMPNPASLLINPLQFPDEGNYIVKVNIGQNGTSLASQKIQTVDVDPVK 136
Qy 115 PQVLV-ASTTVLELSEAFITLNCSENGTKPSYTWLKGKPLNDSRMLLSPDQKVLITR 173
Db 137 PVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSTYSFSPQNTLTIAP 196
Qy 174 VLMEDDDLVSCMVENPISQGRSLPVKITVY 203
Db 197 VTKEIDIGNYCLVRNPVSEMSDIIMPIIY 226

RESULT 3
US-09-902-775A-320

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; Sequence 320, Application US/09902775A
; Patent No. 6686451.
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 320
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-902-775A-320

; Query Match 13.7%; Score 268; DB 4; Length 450;
; Best Local Similarity 31.9%; Pred. No. 1.4e-13;
; Matches 67; Conservative 43; Mismatches 90; Indels 10; Gaps 7;

Qy 1 VNITSPVRLIHGTGKALLSVQYS--STSDRPVVKWQLKR--DKPVTVVQSIGTEVIG 56
Db 20 LKVTVPSTHVGVGRGQALYLPVHYGFHTPASDIQII-WLPERPHTMPKYLGLSVNKSVPV 78

Qy 57 TLRPDYDRIRLF-ENGSLLSLDLQADEGTYEVEISIT-DDTTGKTNILTVDVPISR 114
Db 79 DL--EYQHKFTMPNPASLLINPLQFPDEGNYIYKVNIOGNGTILSASOKIQVTVDVPTK 136

Qy 115 POVLV-ASTTVLELSEAFILNCSHENGTKPSYTWLKDGPCLLNDRLMLLSPDQKVLITR 173
Db 137 PVQIHPPSGAVEYVGNMTLTCHEVGGRTRLAYQWLKNGRPVHTSTSTYSFSPQNNTLHAP 196

Qy 174 VLMEDDDLYSOMVENPISQGRSLPVKITVY 203
Db 197 VTKEIDIGNYSLVRNPVSEMSDIIMPIY 226

RESULT 4
US-09-906-700-320
; Sequence 320, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,700
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
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; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 320
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-700-320

Query Match      13.7%   Score 268;   DB 4;   Length 450;
Best Local Similarity 31.9%;   Pred. No. 1.4e-13;
Matches 67;   Conservative 43;   Mismatches 90;   Indels 10;   Gaps 7;

Qy  1  VNITSPVRLIHGTGKSAALLSVQYS--STSSDRPVVKWQLKR--DKPVTVVQSIGTEVIG 56
Db  20  LKVTVPSTVHVGQALPLPVHYGFHTPASDIQII-WLPERPHTMPKYLGSVNKSVVP 78
Qy  57  TLRPDYDRIRLP-ENGSLLLSDLOADEGTYEVEISIT-DDTFTGKTNLTVDVPISR 114
Db  79  DL--EYQHKFTMPNPASLLINPLQFPDEGNIYVKVNIQNGTLSASQKIQTVDVDPVK 136
Qy  115  PQVLV-ASTTVLELSEAFNLCSHENGTKPSYTWLKDGPPLNDRLMSSPQDKVLTITR 173
Db  137  PVQIHPPSGAVEYVGNWTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFSPQNTLHIAP 196
Qy  174  VLMEDDDLYSWMENPISQGRSLPVKITVY 203
Db  197  VTKEDIGNYCLVRNPVSEMSDIIMPIIY 226

RESULT 5
US-09-903-603A-320
; Sequence 320, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
```

```
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: GNE.1618P2C12
; CURRENT APPLICATION NUMBER: US/09/903,603A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
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; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 320
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-903-603A-320

Query Match      13.7%   Score 268;   DB 4;   Length 450;
Best Local Similarity 31.9%;   Pred. No. 1.4e-13;
Matches 67;   Conservative 43;   Mismatches 90;   Indels 10;   Gaps 7;

Qy  1  VNITSPVRLIHGTGKSAALLSVQYS--STSSDRPVVKWQLKR--DKPVTVVQSIGTEVIG 56
Db  20  LKVTVPSTVHVGQALPLPVHYGFHTPASDIQII-WLPERPHTMPKYLGSVNKSVVP 78
Qy  57  TLRPDYDRIRLP-ENGSLLLSDLOADEGTYEVEISIT-DDTFTGKTNLTVDVPISR 114
Db  79  DL--EYQHKFTMPNPASLLINPLQFPDEGNIYVKVNIQNGTLSASQKIQTVDVDPVK 136
Qy  115  PQVLV-ASTTVLELSEAFNLCSHENGTKPSYTWLKDGPPLNDRLMSSPQDKVLTITR 173
Db  137  PVQIHPPSGAVEYVGNWTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFSPQNTLHIAP 196
Qy  174  VLMEDDDLYSWMENPISQGRSLPVKITVY 203
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RESULT 6
US-09-904-920A-320
; Sequence 320, Application US/09904920A
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; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 320
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-909-064-320

Query Match      13.7%; Score 268; DB 4; Length 450;
Best Local Similarity 31.9%; Pred. No. 1.4e-13;
Matches 67; Conservative 43; Mismatches 90; Indels 10; Gaps 7;

Qy 1 VNITSPVRLIHGTGKSAALLSVQYS--STSDRPVVKWQLKR--DKPVTVVQSIGTEVIG 56
Db 20 LKVTVPSTHTVHGVRGQALYLPVHYGHTPASDIQII-WLFRPHTMPKYLGSVNVKSVVP 78

Qy 57 TLRPDYDRIRLP-ENGSLLSLDLQADGTYEVEISIT-DDTFTGKTNLTVDVPIR 114
Db 79 DL--EYQHKFTMPNPASLLINPLQFPDEGNYIVKVNIOGNGTSLASQKIQTVDVDFVK 136

Qy 115 PQVLV-ASTTVLESEAFNLCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITR 173
Db 137 PVQIHPPSGAVEYVGNMILTCHVEGGTRLAYQWLKNGRPVHTSTSYSFSPQNTLHIAP 196

Qy 174 VLMEDDDLYSVMENPISQGRSLPVKITVY 203
Db 197 VTKEIDIGNYSLVRNPVSEMSDIIMPIIY 226

RESULT 8
US-09-905-381A-320
; Sequence 320, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,381A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 320
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-905-381A-320

Query Match      13.7%; Score 268; DB 4; Length 450;
Best Local Similarity 31.9%; Pred. No. 1.4e-13;
Matches 67; Conservative 43; Mismatches 90; Indels 10; Gaps 7;

Qy 1 VNITSPVRLIHGTGKSAALLSVQYS--STSDRPVVKWQLKR--DKPVTVVQSIGTEVIG 56
Db 20 LKVTVPSTHTVHGVRGQALYLPVHYGHTPASDIQII-WLFRPHTMPKYLGSVNVKSVVP 78

Qy 57 TLRPDYDRIRLP-ENGSLLSLDLQADGTYEVEISIT-DDTFTGKTNLTVDVPIR 114
Db 79 DL--EYQHKFTMPNPASLLINPLQFPDEGNYIVKVNIOGNGTSLASQKIQTVDVDFVK 136

Qy 115 PQVLV-ASTTVLESEAFNLCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITR 173
Db 137 PVQIHPPSGAVEYVGNMILTCHVEGGTRLAYQWLKNGRPVHTSTSYSFSPQNTLHIAP 196

Qy 174 VLMEDDDLYSVMENPISQGRSLPVKITVY 203
Db 197 VTKEIDIGNYSLVRNPVSEMSDIIMPIIY 226

RESULT 9
US-09-906-618-320
; Sequence 320, Application US/09906618
; Patent No. 6828146
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Best Local Similarity 31.9%; Pred. No. 1.4e-13;
Matches 67; Conservative 43; Mismatches 90; Indels 10; Gaps 7

QY 1 WNTSPVRLHGTGKSGALLSVQYS--STSSDRPFWKWKOLKR--DKPVTVVQSIGTEVIG 56
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 20 LKVTVPSTHVGVRGQALYLPVHVGFTHPASDIQII-WLFRPHTMPKYLGSVNKSVP 78
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 57 TLRPDYDRIRLF-ENGSLLLSDIQLADEGTYEVEISIT-DDTFTGEKTNLTVDVPISR 114
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 79 DL--EYQHKFTMPNPASLLINLPQFPDEGNYIVKVNIGQNGTILSASQKIQVTVDDPVTK 136
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 115 POVLV-ASTTVLELSEAFTLNCSHENGTKSPSYTWLKGKPLNDSRMLLSPDQKVLITR 173
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 137 PVWQIHPPSGAVEYVGNNTTCTHVEGTRLAYQWLKNGRPVHTSTYSFSPQNTLTIAP 196
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 174 VLMEDDLLYSQMVENPISQGRSLRPVKITVY 203
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 197 VTREDIGNYSLVRNPFVSEMSDIIMPIY 226
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
US-08-466-465-6
; Sequence 6, Application US/08466465
; Patent No. 6182432
; GENERAL INFORMATION:
; APPLICANT: Wallner, Barbara P.
; TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen
; TITLE OF INVENTION: Presenting Cell Driven Skin Conditions Using
; TITLE OF INVENTION: Inhibitors of the CD2/LFA-3 Interaction
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,465
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/08755
; FILING DATE: 06-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/862,022
; FILING DATE: 12-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/770,969
; FILING DATE: 07-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis (PLM)
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: BGP-111CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-465-6

Query Match 11.1%; Score 218.5; DB 3; Length 351;
Best Local Similarity 23.6%; Pred. No. 1.1e-09;
Matches 81; Conservative 53; Mismatches 148; Indels 61; Gaps 11;

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;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-986-485-2

Query Match      10.2%; Score 199.5; DB 3; Length 1101;
Best Local Similarity 21.3%; Pred. No. 1.9e-07;
Matches 84; Conservative 58; Mismatches 160; Indels 93; Gaps 13;

Qy 13 TVGKALLSVQYSTSDRPVVKQKDKKPVTVVQSIGTEVIGITLDPYDRIRLF--- 69
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 617 TIRTTVARLECAATGHPNOLAWQ---KDG-----GTDPFAKER-RMHVP 660
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 70 ENGSLLSDLQADAGEYVEISITDDTFTGKTIINTVDVPIGRPQVLVASTTVLELSE 129
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 661 DDDVFFITDKIDDAGVY----SCTAQSAGSISANATLTVLEPVLVPLEDRVSVGE 716
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 130 AFTLNCSHENGTKPSYTWLKGKPLNDSRMLLSPDQKVLITITVLMEDDDDLYSCMVENP 189
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 717 TVALQCKATGNPPPRITWFKGDRPLSLTERHHLTPDNQLLVQNVVAEDAGRYTCMSNT 776
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 190 ISQGRSLPVKITVYRRSLYLITSG-----GIF-----LLVTLTVVCACWKPS 233
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 777 LGTERA-----HSQSLVPAAGCKGKTGTVGIFTIAVSSIVLTSLVWVCIIYQTR 827
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 234 KRQKLEKQNSLEYMDQNDRLKPEADTLPRSGEQRKNPMALYILKDKSPETE---E 290
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 828 KKSE-----EYSVNTDETVPDPVPSYLSQGTLSDRQETVVRTEGGPOANGHIE 878
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 291 NPAPEPSATE-PGPGYVSPVAVGRSPGL-----PIRSARR----- 327
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 879 SNGVCPRDASHFPEDTHSVACROPKLCAGSAHYHKEPWKAMEKAEGTPGPHKMEHGRVV 938
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 328 -----YPRSPARSPATGRTHSSPPRAPSSP 352
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 939 CSDCNTEVDCYSRGOAFHPQVSRDSAQPSAPNGP 973
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
US-09-175-928-2
; Sequence 2, Application US/09175928A
; Patent No. 6312921
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Mi, Sha
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 6006B-AJ172A
; CURRENT APPLICATION NUMBER: US/09/175,928A
; CURRENT FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-175-928-2

Query Match      10.0%; Score 196.5; DB 3; Length 387;
Best Local Similarity 24.4%; Pred. No. 7.4e-08;
Matches 82; Conservative 66; Mismatches 151; Indels 37; Gaps 17;

Qy 1 VNITSPVRLHGTGKSAALLSVQYST---SSDRPVVKQL---KRDKEPTVTVQSIGTEVI 55
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 22 VQVTPDGEVNVTVGSNVTLCITVTVASREQLSIQWSPFHKKEMEPISLIYFSGGQAV 81
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 56 GTLRPDYDRIRLPE---NGSLLSLDLQADAGEYVEISITDDTFTGK---TTLNLTVDV 110
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-986-485-2

Query Match      9.9%; Score 195; DB 4; Length 316;
Best Local Similarity 23.4%; Pred. No. 7.4e-08;
Matches 75; Conservative 60; Mismatches 138; Indels 48; Gaps 17;

Qy 1 VNITSPVRLHGTGKSAALLSVQYSTSDRPVVKWQLKRDKEPTVTVQSIGTEVI-GTL 58
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 59 RPDYDRIRLFEFEN-----GSLLSLDLQADAGEYVEISITDDTFTGK---INTVDVPI 112
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 82 ---YKNRVSISNNAEQSDASITIDQLTMADNGTYECSVLSMDLEGNTKSRVRLVLP 138
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 113 SRQVLVASTTVLELSEAFPLNC-SHENGTKPSYTWLKGKPLNDSRMLLSP-DQKVL 170
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 139 SKPECGIEGETI--IGNNIQLTCQSKGSPTPQSWKRYN--ILNQQLAQPASGQPS 194
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 171 ITRVLMEDDDDLYSCMVENPISQGRSLPVKITVYRRS-----SLYIILSTGSI--FLAVTL 223
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 195 LKNISTDTSGYIYCTSSN--EEGTQF-CNITVAVRSPSMVALYVAVGAVVAAIIIGI 251
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 224 VTVCAWKPSKRQKKLEKQNSLEYMDQNDRLKPEADTLPRSGEQRKNPMALYILKDK 283
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 252 IIVCCCR-----GKDDNTE--DKEDAR--PNREAYEEPEQLRE-----LSR 290
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 284 DSPETEENPAPEPRSATTEPGP 304
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 291 EREEDDYRQEQKSTGRESP 311
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
US-08-597-495B-22
; Sequence 22, Application US/08597495B
; Patent No. 5713369
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 16:01:42 ; Search time 98.0554 Seconds
(without alignments)
1519.387 Million cell updates/sec

Title: US-10-706-691-26
Perfect score: 1962
Sequence: 1 VNITSPVRLHGTGKSAALL.....TAGVHIHQEAGPVEISA 383

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 38892284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1962	100.0	383	16	US-10-706-691-26
2	1962	100.0	416	16	US-10-706-691-16
3	1962	100.0	416	16	US-10-706-691-41
4	1850	94.3	418	16	US-10-706-691-18
5	1312	66.9	298	15	US-10-432-103-4
6	1157	59.0	224	15	US-10-415-188-7
7	1045	53.3	207	16	US-10-706-691-22
8	1045	53.3	240	16	US-10-706-691-20
9	1045	53.3	246	16	US-10-706-691-43
10	1029	52.4	256	15	US-10-112-944-434
11	1018	51.9	256	15	US-10-112-944-880
					Sequence 26, Appl
					Sequence 16, Appl
					Sequence 41, Appl
					Sequence 18, Appl
					Sequence 7, Appl
					Sequence 22, Appl
					Sequence 20, Appl
					Sequence 43, Appl
					Sequence 434, Appl
					Sequence 880, Appl

12	548	27.9	110	16	US-10-706-691-24	Sequence 24, Appl
13	548	27.9	114	16	US-10-706-691-4	Sequence 4, Appl
14	522	26.6	100	16	US-10-706-691-14	Sequence 14, Appl
15	484	24.7	94	16	US-10-706-691-6	Sequence 6, Appl
16	268	13.7	450	9	US-09-909-320-320	Sequence 320, Appl
17	268	13.7	450	9	US-09-909-088B-320	Sequence 320, Appl
18	268	13.7	450	9	US-09-905-291A-320	Sequence 320, Appl
19	268	13.7	450	9	US-09-902-853-320	Sequence 320, Appl
20	268	13.7	450	9	US-09-907-824-320	Sequence 320, Appl
21	268	13.7	450	9	US-09-907-841-320	Sequence 320, Appl
22	268	13.7	450	10	US-09-904-011-320	Sequence 320, Appl
23	268	13.7	450	10	US-09-903-640-320	Sequence 320, Appl
24	268	13.7	450	10	US-09-908-093-320	Sequence 320, Appl
25	268	13.7	450	10	US-09-906-742-320	Sequence 320, Appl
26	268	13.7	450	10	US-09-906-838-320	Sequence 320, Appl
27	268	13.7	450	10	US-09-907-613-320	Sequence 320, Appl
28	268	13.7	450	10	US-09-907-942-320	Sequence 320, Appl
29	268	13.7	450	10	US-09-904-859-320	Sequence 320, Appl
30	268	13.7	450	10	US-09-909-204-320	Sequence 320, Appl
31	268	13.7	450	10	US-09-904-820-320	Sequence 320, Appl
32	268	13.7	450	10	US-09-904-786-320	Sequence 320, Appl
33	268	13.7	450	10	US-09-906-646-320	Sequence 320, Appl
34	268	13.7	450	10	US-09-906-700-320	Sequence 320, Appl
35	268	13.7	450	10	US-09-902-903-320	Sequence 320, Appl
36	268	13.7	450	10	US-09-903-786-320	Sequence 320, Appl
37	268	13.7	450	10	US-09-903-749A-320	Sequence 320, Appl
38	268	13.7	450	10	US-09-904-119-320	Sequence 320, Appl
39	268	13.7	450	10	US-09-904-956-320	Sequence 320, Appl
40	268	13.7	450	10	US-09-902-736-320	Sequence 320, Appl
41	268	13.7	450	10	US-09-907-794-320	Sequence 320, Appl
42	268	13.7	450	10	US-09-903-943-320	Sequence 320, Appl
43	268	13.7	450	10	US-09-904-462-320	Sequence 320, Appl
44	268	13.7	450	10	US-09-907-925-320	Sequence 320, Appl
45	268	13.7	450	10	US-09-902-692-320	Sequence 320, Appl

ALIGNMENTS

RESULT 1

US-10-706-691-26
; Sequence 26, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fegan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boeschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 26
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-26

Query Match 100.0%; Score 1962; DB 16; Length 383;
Best Local Similarity 100.0%; Pred. No. 9.6e-127;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VNITSPVRLHGTGKSAALLSVQSTSSDRPVVVKQLKDKPVTVVQSIGTIGTLRP 60
Db 1 VNITSPVRLHGTGKSAALLSVQSTSSDRPVVVKQLKDKPVTVVQSIGTIGTLRP 60

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QY 61 DYDRIRLFENGSLLSLDQLADGTYEVEISITDDTFTGKTNLTVDVPISRPQVLVA 120
DB 61 DYDRIRLFENGSLLSLDQLADGTYEVEISITDDTFTGKTNLTVDVPISRPQVLVA 120
QY 121 STTVLELSEAFNLCSHENGTKPSYTWLKDGPFLNDSRMLLSPDQKVLITITVLMEDDD 180
DB 121 STTVLELSEAFNLCSHENGTKPSYTWLKDGPFLNDSRMLLSPDQKVLITITVLMEDDD 180
QY 181 LYSWENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCAWKPSKRKOKKL 240
DB 181 LYSWENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCAWKPSKRKOKKL 240
QY 241 EKQNSLEYMDQNDRLKPEADTLPRSGEQERKNPMALYIILKDKDSPETENPAPEPSAT 300
DB 241 EKQNSLEYMDQNDRLKPEADTLPRSGEQERKNPMALYIILKDKDSPETENPAPEPSAT 300
QY 301 EPQPPGYSVSPAVGPGSPGLPIRSARRYPRSPARSPATGTHSSPPRAPSSPGRSRSASR 360
DB 301 EPQPPGYSVSPAVGPGSPGLPIRSARRYPRSPARSPATGTHSSPPRAPSSPGRSRSASR 360
QY 361 TLRTAGVHIIREODEAGPVEISA 383
DB 361 TLRTAGVHIIREODEAGPVEISA 383

RESULT 2
US-10-706-691-16
; Sequence 16, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 16
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-16

Query Match 100.0%; Score 1962; DB 16; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.1e-126;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNITSPVRLIHGTGKSALLSVQYSSTSDRPVVKWLKRDKPVTVVQSIGTEVIGTLRP 60
DB 34 VNITSPVRLIHGTGKSALLSVQYSSTSDRPVVKWLKRDKPVTVVQSIGTEVIGTLRP 93
QY 61 DYDRIRLFENGSLLSLDQLADGTYEVEISITDDTFTGKTNLTVDVPISRPQVLVA 120
DB 94 DYDRIRLFENGSLLSLDQLADGTYEVEISITDDTFTGKTNLTVDVPISRPQVLVA 153
QY 121 STTVLELSEAFNLCSHENGTKPSYTWLKDGPFLNDSRMLLSPDQKVLITITVLMEDDD 180
DB 154 STTVLELSEAFNLCSHENGTKPSYTWLKDGPFLNDSRMLLSPDQKVLITITVLMEDDD 213
QY 181 LYSWENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCAWKPSKRKOKKL 240
DB 214 LYSWENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCAWKPSKRKOKKL 273
QY 241 EKQNSLEYMDQNDRLKPEADTLPRSGEQERKNPMALYIILKDKDSPETENPAPEPSAT 300
DB 274 EKQNSLEYMDQNDRLKPEADTLPRSGEQERKNPMALYIILKDKDSPETENPAPEPSAT 333
QY 301 EPQPPGYSVSPAVGPGSPGLPIRSARRYPRSPARSPATGTHSSPPRAPSSPGRSRSASR 360
DB 334 EPQPPGYSVSPAVGPGSPGLPIRSARRYPRSPARSPATGTHSSPPRAPSSPGRSRSASR 393
QY 361 TLRTAGVHIIREODEAGPVEISA 383
DB 394 TLRTAGVHIIREODEAGPVEISA 416
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QY 241 EKQNSLEYMDQNDRLKPEADTLPRSGEQERKNPMALYIILKDKDSPETENPAPEPSAT 300
DB 274 EKQNSLEYMDQNDRLKPEADTLPRSGEQERKNPMALYIILKDKDSPETENPAPEPSAT 333
QY 301 EPQPPGYSVSPAVGPGSPGLPIRSARRYPRSPARSPATGTHSSPPRAPSSPGRSRSASR 360
DB 334 EPQPPGYSVSPAVGPGSPGLPIRSARRYPRSPARSPATGTHSSPPRAPSSPGRSRSASR 393
QY 361 TLRTAGVHIIREODEAGPVEISA 383
DB 394 TLRTAGVHIIREODEAGPVEISA 416

RESULT 3
US-10-706-691-41
; Sequence 41, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 41
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-41

Query Match 100.0%; Score 1962; DB 16; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.1e-126;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNITSPVRLIHGTGKSALLSVQYSSTSDRPVVKWLKRDKPVTVVQSIGTEVIGTLRP 60
DB 34 VNITSPVRLIHGTGKSALLSVQYSSTSDRPVVKWLKRDKPVTVVQSIGTEVIGTLRP 93
QY 61 DYDRIRLFENGSLLSLDQLADGTYEVEISITDDTFTGKTNLTVDVPISRPQVLVA 120
DB 94 DYDRIRLFENGSLLSLDQLADGTYEVEISITDDTFTGKTNLTVDVPISRPQVLVA 153
QY 121 STTVLELSEAFNLCSHENGTKPSYTWLKDGPFLNDSRMLLSPDQKVLITITVLMEDDD 180
DB 154 STTVLELSEAFNLCSHENGTKPSYTWLKDGPFLNDSRMLLSPDQKVLITITVLMEDDD 213
QY 181 LYSWENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCAWKPSKRKOKKL 240
DB 214 LYSWENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCAWKPSKRKOKKL 273
QY 241 EKQNSLEYMDQNDRLKPEADTLPRSGEQERKNPMALYIILKDKDSPETENPAPEPSAT 300
DB 274 EKQNSLEYMDQNDRLKPEADTLPRSGEQERKNPMALYIILKDKDSPETENPAPEPSAT 333
QY 301 EPQPPGYSVSPAVGPGSPGLPIRSARRYPRSPARSPATGTHSSPPRAPSSPGRSRSASR 360
DB 334 EPQPPGYSVSPAVGPGSPGLPIRSARRYPRSPARSPATGTHSSPPRAPSSPGRSRSASR 393
QY 361 TLRTAGVHIIREODEAGPVEISA 383
DB 394 TLRTAGVHIIREODEAGPVEISA 416
```

RESULT 4

US-10-706-691-18
; Sequence 18, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10/706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 18
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-18

Query Match 94.3%; Score 1850; DB 16; Length 418;

Best Local Similarity 94.5%; Pred. No. 5.4e-119;

Matches 364; Conservative 9; Mismatches 10; Indels 2; Gaps 1;

Qy	1	WNITSPVRLIHGTGKSA	LLSVQSS	TSDDRPVVKWLKRD	KPVTVVQSIGTEVIGTLRP	60	
Db	34	WNITSPVRLIHGTGKSA	LLSVQSS	TSDDRPVVKWLKRD	KPVTVVQSIGTEVIGTLRP	93	
Qy	61	DYRDIRLFENGSL	LLSDQLADEGTYE	VEISITDDTFTG	EKTINLTVDVPISRPQVLVA	120	
Db	94	DYRDIRLFENGSL	LLSDQLADEGTYE	VEISITDDTFTG	EKTINLTVDVPISRPQVLVA	153	
Qy	121	STTVLESEAF	TNCNCSHENG	TKPSYTWLKD	KPLNDSRM	LLSPDQKVLITITRVL	180
Db	154	STTVLESEAF	TNCNCSHENG	TKPSYTWLKD	KPLNDSRM	LLSPDQKVLITITRVL	213
Qy	181	LYSCWENPISQ	GRSLPVKITVY	RRSSLYIIL	STGGIFLLV	TVTVCAWKPSK	238
Db	214	LYSCWENPISQ	GRSLPVKITVY	RRSSLYIIL	STGGIFLLV	TVTVCAWKPSK	273
Qy	239	KLEKNSLEYMD	QNDRLKPEAD	TLPRSGEQER	KNPWALYIL	KDKSPETEEN	298
Db	274	KLEKNSLEYMD	QNDRLKPEAD	TLPRSGEQER	KNPWALYIL	KDKSPETEEN	333
Qy	299	ATERGPGYSV	SPVPGPSGLP	TRSARRYP	SPSPATGRT	HSSPPRAP	358
Db	334	ATERGPGYSV	SPVPGPSGLP	TRSARRYP	SPSPATGRT	HSSPPRAP	393
Qy	359	SRTLRTAGV	HTIREQD	AGPVEISA	383		
Db	394	SRTLRTAGV	HTIREQD	AGPVEISA	418		

RESULT 5

US-10-432-103-4
; Sequence 4, Application US/10432103
; Publication No. US20040043424A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: YUE, Henry
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: THANGAVELOU, Kavitha
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: LU, Yan

; APPLICANT: LO, Terrence P.
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: GANDHI, Ameen R.
; APPLICANT: ARVIZU, Chandra
; APPLICANT: YAO, Monique G.
; TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS
; FILE REFERENCE: PF-0841 PCT
; CURRENT APPLICATION NUMBER: US/10/432,103
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: 60/249,645
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040043424A1 5831801CD1
US-10-432-103-4

Query Match 66.9%; Score 1312; DB 15; Length 298;

Best Local Similarity 100.0%; Pred. No. 3.6e-82;

Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	WNITSPVRLIHGTGKSA	LLSVQSS	TSDDRPVVKWLKRD	KPVTVVQSIGTEVIGTLRP	60	
Db	34	WNITSPVRLIHGTGKSA	LLSVQSS	TSDDRPVVKWLKRD	KPVTVVQSIGTEVIGTLRP	93	
Qy	61	DYRDIRLFENGSL	LLSDQLADEGTYE	VEISITDDTFTG	EKTINLTVDVPISRPQVLVA	120	
Db	94	DYRDIRLFENGSL	LLSDQLADEGTYE	VEISITDDTFTG	EKTINLTVDVPISRPQVLVA	153	
Qy	121	STTVLESEAF	TNCNCSHENG	TKPSYTWLKD	KPLNDSRM	LLSPDQKVLITITRVL	180
Db	154	STTVLESEAF	TNCNCSHENG	TKPSYTWLKD	KPLNDSRM	LLSPDQKVLITITRVL	213
Qy	181	LYSCWENPISQ	GRSLPVKITVY	RRSSLYIIL	STGGIFLLV	TVTVCAWKPSK	240
Db	214	LYSCWENPISQ	GRSLPVKITVY	RRSSLYIIL	STGGIFLLV	TVTVCAWKPSK	273
Qy	241	EKNSLEYMD	QNDRLKP	258			
Db	274	EKNSLEYMD	QNDRLKP	291			

RESULT 6
US-10-415-188-7
; Sequence 7, Application US/10415188
; Publication No. US20040049010A1
; GENERAL INFORMATION:
; APPLICANT: WARREN, Bridget A.; XU, Yuming;
; APPLICANT: YUE, Henry; BATRA, Sajeev;
; APPLICANT: BURFORD, Neil; GANDHI, Ameen R.;
; APPLICANT: CHAWLA, Narinder K.; ARVIZU, Chandra S.;
; APPLICANT: TANG, Y. Tom; LU, Dyung Aina M.;
; APPLICANT: DUGGAN, Brendan M.; BAUGHN, Mariah R.;
; APPLICANT: LEE, Ernestine A.; KHAN, Farrah A.;
; APPLICANT: NGUYEN, Damiel B.; AZIMZAI, Yalda;
; APPLICANT: YAO, Monique G.; LAL, Preeti G.;
; APPLICANT: THANGAVELOU, Kavitha; RAMKUMAR, Jayalaxmi;
; APPLICANT: TRAN, Bao; DING, Li;
; APPLICANT: AU-YOUNG, Janice
; TITLE OF INVENTION: TRANSMEMBRANE PROTEINS
; FILE REFERENCE: PF-0836 USN
; CURRENT APPLICATION NUMBER: US/10/415,188
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: PCT/US01/49670
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/244,017
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/252,855

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; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/251,825
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/255,085
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: incyte ID No. US20040049010A1 382654CD1
; US-10-415-188-7

Query Match      59.0%; Score 1157; DB 15; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.2e-71;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 160 MLLSPDQKVLITITVLMEDDDLLYSCMVENPISQGRSLPVKITVYRRSLYIILSTGGIFL 219
Db 1 MLLSPDQKVLITITVLMEDDDLLYSCMVENPISQGRSLPVKITVYRRSLYIILSTGGIFL 60
Qy 220 LVTLVTVACWPKSRKQKLEKONSLEYMDQNDRLKPEADTLPRSGEERKNPMALYI 279
Db 61 LVTLVTVACWPKSRKQKLEKONSLEYMDQNDRLKPEADTLPRSGEERKNPMALYI 120
Qy 280 LKQKDSPEETENPAPEPRSPATEPGPGYGSVPVPGSRPGLPIRSARRYPRSPARSPATG 339
Db 121 LKQKDSPEETENPAPEPRSPATEPGPGYGSVPVPGSRPGLPIRSARRYPRSPARSPATG 180
Qy 340 RTHSSPPRAPSSPGRSRSASRTLRTAGVHIIREQDEAGPVEISA 383
Db 181 RTHSSPPRAPSSPGRSRSASRTLRTAGVHIIREQDEAGPVEISA 224

RESULT 7
US-10-706-691-22
; Sequence 22, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10/706,691
; PRIOR FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 22
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-706-691-22

Query Match      53.3%; Score 1045; DB 16; Length 240;
Best Local Similarity 100.0%; Pred. No. 5.4e-64;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNITSPVRLIHGTGKSAALLSVQYSSSTSDRPVVKQKRDKPVTVVQSIGTEVIGTLRP 60
Db 34 VNITSPVRLIHGTGKSAALLSVQYSSSTSDRPVVKQKRDKPVTVVQSIGTEVIGTLRP 93
Qy 61 DYDRIRLRFENGSLILLSDLQLADEGTVEVEISITDDTFTGKKTINLTVDPISRPOVLVA 120
Db 94 DYDRIRLRFENGSLILLSDLQLADEGTVEVEISITDDTFTGKKTINLTVDPISRPOVLVA 153
Qy 121 STTVLELSEAFITLNCSHENGTKPSYTWLKDGPILLNDSRMLLSPDQKVLITITVLMEDDD 180
Db 154 STTVLELSEAFITLNCSHENGTKPSYTWLKDGPILLNDSRMLLSPDQKVLITITVLMEDDD 213
Qy 181 LYSQMVENPISQGRSLPVKITVYRRSS 207
Db 214 LYSQMVENPISQGRSLPVKITVYRRSS 240

RESULT 8
US-10-706-691-20
; Sequence 20, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10/706,691
; PRIOR FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 20
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-706-691-20

Query Match      53.3%; Score 1045; DB 16; Length 240;
Best Local Similarity 100.0%; Pred. No. 6.5e-64;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNITSPVRLIHGTGKSAALLSVQYSSSTSDRPVVKQKRDKPVTVVQSIGTEVIGTLRP 60
Db 34 VNITSPVRLIHGTGKSAALLSVQYSSSTSDRPVVKQKRDKPVTVVQSIGTEVIGTLRP 93
Qy 61 DYDRIRLRFENGSLILLSDLQLADEGTVEVEISITDDTFTGKKTINLTVDPISRPOVLVA 120
Db 94 DYDRIRLRFENGSLILLSDLQLADEGTVEVEISITDDTFTGKKTINLTVDPISRPOVLVA 153
Qy 121 STTVLELSEAFITLNCSHENGTKPSYTWLKDGPILLNDSRMLLSPDQKVLITITVLMEDDD 180
Db 154 STTVLELSEAFITLNCSHENGTKPSYTWLKDGPILLNDSRMLLSPDQKVLITITVLMEDDD 213
Qy 181 LYSQMVENPISQGRSLPVKITVYRRSS 207
Db 214 LYSQMVENPISQGRSLPVKITVYRRSS 240

RESULT 9
US-10-706-691-43
; Sequence 43, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; US-10-706-691-43

Query Match      53.3%; Score 1045; DB 16; Length 207;
Best Local Similarity 100.0%; Pred. No. 5.4e-64;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNITSPVRLIHGTGKSAALLSVQYSSSTSDRPVVKQKRDKPVTVVQSIGTEVIGTLRP 60
Db 1 VNITSPVRLIHGTGKSAALLSVQYSSSTSDRPVVKQKRDKPVTVVQSIGTEVIGTLRP 60
Qy 61 DYDRIRLRFENGSLILLSDLQLADEGTVEVEISITDDTFTGKKTINLTVDPISRPOVLVA 120
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; CURRENT APPLICATION NUMBER: US/10/706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 43
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-43

Query Match      53.3%; Score 1045; DB 16; Length 246;
Best Local Similarity 100.0%; Pred. No. 6.7e-64;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNITSPVRLIHGTGKSAALLSVQYSSSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 60
Db 34 VNITSPVRLIHGTGKSAALLSVQYSSSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 93

Qy 61 DYDRIRLRFENGSLLLSDQLADEGTVEVEISITDDTFTGKTNLTVDPISRPQVLVA 120
Db 94 DYDRIRLRFENGSLLLSDQLADEGTVEVEISITDDTFTGKTNLTVDPISRPQVLVA 153

Qy 121 STTVLELSEAFTLNCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDDD 180
Db 154 STTVLELSEAFTLNCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDDD 213

Qy 181 LYSQWENPISQGRSLPKITVYRRSS 207
Db 214 LYSQWENPISQGRSLPKITVYRRSS 240

RESULT 10
US-10-112-944-434
; Sequence 434, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: Pt_FL_genes Version 5.0
; SEQ ID NO 880
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens

; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: pt_FL_genes Version 5.0
; SEQ ID NO 434
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-112-944-434

Query Match      52.4%; Score 1029; DB 15; Length 256;
Best Local Similarity 96.2%; Pred. No. 8.9e-63;
Matches 203; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VNITSPVRLIHGTGKSAALLSVQYSSSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 60
Db 34 VNITSPVRLIHGTGKSAALLSVQYSSSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 93

Qy 61 DYDRIRLRFENGSLLLSDQLADEGTVEVEISITDDTFTGKTNLTVDPISRPQVLVA 120
Db 94 DYDRIRLRFENGSLLLSDQLADEGTVEVEISITDDTFTGKTNLTVDPISRPQVLVA 153

Qy 121 STTVLELSEAFTLNCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDDD 180
Db 154 STTVLELSEAFTLNCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDDD 213

Qy 181 LYSQWENPISQGRSLPKITVYRRSSLYII 211
Db 214 LDCVVENPINQGRTLPECKITVYKSSFYII 244

RESULT 11
US-10-112-944-880
; Sequence 880, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: Pt_FL_genes Version 5.0
; SEQ ID NO 880
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-112-944-880

Query Match 51.9%; Score 1018; DB 15; Length 256;
Best Local Similarity 96.6%; Pred. No. 5.1e-62;
Matches 201; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNITSPVRLIHGTGKSAALLSVQSSSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 60
DB 34 VNITSPVRLIHGTGKSAALLSVQSSSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 93

QY 61 DYDRIRLRFENGSLLSLSDQLADSGTYEVEISITDDTFTGKKTINLTVDVPIRQPVLVA 120
DB 94 DYDRIRLRFENGSLLSLSDQLADSGTYEVEISITDDTFTGKKTINLTVDVPIRQPVLGA 153

QY 121 STTVLELSEAFTLNCSENGTKPSYTWLKGKPLNDSRMLLSPDKVLTITRVLMEDDD 180
DB 154 STTVLELSEAFTLNCSENGTKPSYTWLKGKPLNDSRMLLSPDKVLTITRVLMEDDD 213

QY 181 LYSCMVENPISQGRSLPVKITVYRRSSL 208
DB 214 LYSCMVENPINOGRTLPCKITRYKSSSL 241

RESULT 12

US-10-706-691-24
; Sequence 24, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 24
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-24

Query Match 27.9%; Score 548; DB 16; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.8e-30;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNITSPVRLIHGTGKSAALLSVQSSSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 60
DB 1 VNITSPVRLIHGTGKSAALLSVQSSSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 60

QY 61 DYDRIRLRFENGSLLSLSDQLADSGTYEVEISITDDTFTGKKTINLTVDV 110
DB 61 DYDRIRLRFENGSLLSLSDQLADSGTYEVEISITDDTFTGKKTINLTVDV 110

RESULT 13

US-10-706-691-4
; Sequence 4, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande

; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 4
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-4

Query Match 27.9%; Score 548; DB 16; Length 114;
Best Local Similarity 100.0%; Pred. No. 3.9e-30;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNITSPVRLIHGTGKSAALLSVQSSSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 60
DB 5 VNITSPVRLIHGTGKSAALLSVQSSSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 64

QY 61 DYDRIRLRFENGSLLSLSDQLADSGTYEVEISITDDTFTGKKTINLTVDV 110
DB 65 DYDRIRLRFENGSLLSLSDQLADSGTYEVEISITDDTFTGKKTINLTVDV 114

RESULT 14

US-10-706-691-14
; Sequence 14, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 14
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-14

Query Match 26.6%; Score 522; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 2e-28;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 284 DSPETENPAPEPRSATPEPGPGYSVPVPGRSPGLPIRSARRYPSPARSATGRTHS 343
DB 1 DSPETENPAPEPRSATPEPGPGYSVPVPGRSPGLPIRSARRYPSPARSATGRTHS 60

QY 344 SPPRAPSSPCGRSRASRTLTAGVHIIREQDEAGPVEISA 383
DB 61 SPPRAPSSPCGRSRASRTLTAGVHIIREQDEAGPVEISA 100

RESULT 15

US-10-706-691-6
; Sequence 6, Application US/10706691

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; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10/706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 6
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-6

Query Match      24.7%; Score 484; DB 16; Length 94;
Best Local Similarity 100.0%; Pred. No. 7.8e-26;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      111 PISRPQVLVASTTVLELSEAFLLNCSEHNGTKPSYTWLKGKPLINDSRMLLSPDQKVL 170
Db      1 PISRPQVLVASTTVLELSEAFLLNCSEHNGTKPSYTWLKGKPLINDSRMLLSPDQKVL 60

Qy      171 ITRVLMEDDDLYSCMVENPISQGRSLPVKITVYR 204
Db      61 ITRVLMEDDDLYSCMVENPISQGRSLPVKITVYR 94

Search completed: July 26, 2005, 16:21:19
Job time : 99.0554 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 15:54:21 ; Search time 108.506 Seconds
(without alignments)
1365.166 Million cell updates/sec

Title: US-10-706-691-26

Perfect score: 1962

Sequence: 1 VNITSPVRLIHGTGKSALL.....TAGVHIHQDEAGPVEISA 383

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqpl1980s:*
- 2: geneseqpl1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1962	100.0	383	8	ADO47895 Human mat
2	1962	100.0	416	7	Abg75379 Predicted
3	1962	100.0	416	7	Abg75377 Human INS
4	1962	100.0	416	8	ADO47892 Human pro
5	1962	100.0	416	8	ADs11056 Human the
6	1850	94.3	418	7	Abg75378 Murine IN
7	1318.5	67.2	367	8	Adg65357 Novel hum
8	1312	66.9	298	5	AAE14784 Human imm
9	1192	60.8	237	8	ADO47890 Human mat
10	1192	60.8	270	8	ADO47887 Human pro
11	1192	60.8	270	8	ADs11055 Human the
12	1157	59.0	224	5	AAE26421 Human tra
13	1045	53.3	246	7	Abg75380 INSP052 e
14	1029	52.4	256	8	Adm87341 Human pro
15	1018	51.9	256	4	RAM24238 Human EST
16	1018	51.9	256	8	Adm87787 Human EST
17	1018	51.9	256	8	ADs112269 Human the
18	1018	51.9	256	8	ADs112268 Human the
19	548	27.9	114	7	Abg75371 Human INS
20	522	26.6	100	7	Abg75376 Human INS
21	484	24.7	188	7	Abg75372 Human INS
22	268	13.7	338	4	RAM79339 Human pro
23	268	13.7	450	2	AAy13398 Amino aci
24	268	13.7	450	3	Adc78632 Human PRO
25	268	13.7	450	4	AAb80266 Human PRO

26	268	13.7	450	4	AAU12360 Human PRO
27	268	13.7	450	5	AAU81958 Human PRO
28	268	13.7	450	6	ABU71644 Human PRO
29	268	13.7	450	6	ABO17804 Novel hum
30	268	13.7	450	6	ABU71499 Human PRO
31	268	13.7	450	6	ABU81058 Human PRO
32	268	13.7	450	6	ABU71945 Human sec
33	268	13.7	450	6	ABO01828 Novel hum
34	268	13.7	450	6	ABU66758 Human PRO
35	268	13.7	450	6	ABU54401 Human sec
36	268	13.7	450	6	ABO47416 Human sec
37	268	13.7	450	6	ABU59839 Novel sec
38	268	13.7	450	6	ABO25029 Human sec
39	268	13.7	450	6	ABU64553 Human sec
40	268	13.7	450	6	ABU67399 Human sec
41	268	13.7	450	6	ABO14919 Human sec
42	268	13.7	450	6	ABU67034 Human sec
43	268	13.7	450	6	ABU69676 Novel hum
44	268	13.7	450	6	ABO14858 Human sec
45	268	13.7	450	6	ADA45897 Novel hum

ALIGNMENTS

RESULT 1

ADO47895
ID ADO47895 standard; protein; 383 AA.

XX AC ADO47895;

XX DT 15-JUL-2004 (first entry)

XX DE Human mature protein SEQ ID NO:12.

XX KW human; viricide; anti-HIV; cytostatic; antiinflammatory; antiallergic; immunosuppressive; antiarteriosclerotic; hypotensive; osteopathic; antianaemic; neuroprotective; nootropic; antiparkinsonian; antiasthmatic; haemostatic; antidiabetic; cardiant; HIV; viral infection; cancer; inflammation; allergy; graft rejection; atherosclerosis; hypertension; osteoporosis; anaemia; Alzheimer's disease; Parkinson's disease; asthma; diabetes; myocardial infarction; haemophilia.

XX OS Homo sapiens.

XX PN WO2004007672-A2.

XX PD 22-JAN-2004.

XX PP 09-JUL-2003; 2003WO-US021703.

XX PR 12-JUL-2002; 2002US-0395402P.

XX PA (NUVE-) NUVELO INC.

XX PI Rupp F, Wang J, Zhou P, Wehrman T, Wang ZW, Tang YT;

XX DR WPI; 2004-122914/12.

XX DR N-PSDB; ADO47893.

XX FT New isolated polypeptides and polynucleotides useful in diagnostics, forensics, in preventing or treating diseases such as HIV and cancer, and as drug targets.

XX PT Claim 10; SEQ ID NO 12; 205pp; English.

XX PS The invention relates to novel isolated polynucleotides and polypeptides encoded by them. Also included are mutants or variants of the polynucleotides and polypeptides. A polypeptide of the invention has viricide, anti-HIV, cytostatic, antiinflammatory, antiallergic, immunosuppressive, antiarteriosclerotic, hypotensive, osteopathic, antianaemic, neuroprotective, nootropic, antiparkinsonian, antiasthmatic, haemostatic, antidiabetic, and cardiant activity. The composition and

CC methods are useful in diagnostics, forensics, gene or chromosome mapping,
 CC identification of mutations responsible for genetic disorders or other
 CC traits, in assessing biodiversity, or in producing many other types of
 CC data and products dependent on DNA and amino acid sequences. They may
 CC also be used in preventing or treating diseases (e.g. HIV and other viral
 CC infections, cancer, inflammation, allergies, graft rejection,
 CC atherosclerosis, hypertension, osteoporosis, anaemia, Alzheimer's
 CC disease, Parkinson's disease, asthma, diabetes, myocardial infarction or
 CC haemophilia). They may also be used as targets in drug screening. The
 CC present sequence represents a polypeptide of the invention.

XX SQ Sequence 383 AA;

Query Match 100.0%; Score 1962; DB 8; Length 383;
 Best Local Similarity 100.0%; Pred. No. 2.7e-134;
 Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNITSPVRLIHGTGKSGALLSVQYSSSTSDRPVVKWQLKRDKPTVVVQSIGTEVIGTLRP 60
 DB |||||
 QY 1 VNITSPVRLIHGTGKSGALLSVQYSSSTSDRPVVKWQLKRDKPTVVVQSIGTEVIGTLRP 60
 DB |||||
 QY 61 DYDRIRLFENGSLLLSDQLADEGTVEVEISITDDTFTGKTNLTVDVPISRPQVLVA 120
 DB |||||
 QY 61 DYDRIRLFENGSLLLSDQLADEGTVEVEISITDDTFTGKTNLTVDVPISRPQVLVA 120
 DB |||||
 QY 121 STTVLEISEAFTLNCSEHGKPSYTWLKDGPPLNDSRMILLSPDQKVLITITVLMEDDD 180
 DB |||||
 QY 121 STTVLEISEAFTLNCSEHGKPSYTWLKDGPPLNDSRMILLSPDQKVLITITVLMEDDD 180
 DB |||||
 QY 181 LYSYCWENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLTVCAWKPSKRQKKL 240
 DB |||||
 QY 181 LYSYCWENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLTVCAWKPSKRQKKL 240
 DB |||||
 QY 241 EKQNSLEYMDQNDRLKPEADTLPRSGEQRKNPMALYILKDKDSPETENPAPEPSAT 300
 DB |||||
 QY 241 EKQNSLEYMDQNDRLKPEADTLPRSGEQRKNPMALYILKDKDSPETENPAPEPSAT 300
 DB |||||
 QY 301 EPGPPGYSVPVPGSRSPGLPIRSARYPRSPARSPATGRTHSSPPRAPSPPGRSRASR 360
 DB |||||
 QY 301 EPGPPGYSVPVPGSRSPGLPIRSARYPRSPARSPATGRTHSSPPRAPSPPGRSRASR 360
 DB |||||
 QY 361 TLRTAGVHIIREQDEAGPVEISA 383
 DB |||||
 QY 361 TLRTAGVHIIREQDEAGPVEISA 383
 DB |||||

RESULT 2

ID ABG75379 standard; protein; 416 AA.

XX AC ABG75379;

XX DT 22-APR-2004 (first entry)

XX DE Predicted INSP052 protein.

XX KW INSP052; human; cell proliferation; autoimmune disease; inflammation;
 KW cardiovascular disease; neurological disease; psychiatric disease;
 KW developmental disease; metabolic disorder; infection;
 KW immunoglobulin domain-containing cell surface recognition molecule.

OS Unidentified.

XX PN WO2003093316-A2.

XX PD 13-NOV-2003.

XX PF 30-APR-2003; 2003WO-GB001851.

XX PR 30-APR-2002; 2002GB-00009884.

XX PA (ARES-) ARES TRADING SA.

XX

PI Davids AR, Fagan RJ, Phelps CB, Power C;

XX WPI; 2003-903655/82.

DR N-PSDB; ACH01277.

XX New INSP052 polypeptides and nucleic acids, useful in diagnosing and
 PT treating cell proliferative, autoimmune/inflammatory, cardiovascular,
 PT neurological, psychiatric, developmental, genetic or metabolic disorder.

XX Example 2; Fig 5; Opp; English.

XX The present invention provides the protein and coding sequences of a
 CC novel human immunoglobulin domain-containing cell surface recognition
 CC molecule known as INSP052. The polypeptide is useful as immunoglobulin
 CC domain-containing cell surface recognition molecule. The sequences may
 CC also be used in therapy or diagnosing a disease or in the manufacture of
 CC a medicament for treating a disease. The disease is a cell proliferative,
 CC autoimmune/inflammatory, cardiovascular, neurological, psychiatric,
 CC developmental, genetic or metabolic disorder, an infection or other
 CC pathological condition. The polypeptides and nucleic acids are essential
 CC to the structural integrity and homeostatic functioning of most tissues.
 CC The present sequence is a polypeptide shown in the invention

XX Sequence 416 AA;

Query Match 100.0%; Score 1962; DB 7; Length 416;
 Best Local Similarity 100.0%; Pred. No. 3e-134;
 Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNITSPVRLIHGTGKSGALLSVQYSSSTSDRPVVKWQLKRDKPTVVVQSIGTEVIGTLRP 60

DB 34 VNITSPVRLIHGTGKSGALLSVQYSSSTSDRPVVKWQLKRDKPTVVVQSIGTEVIGTLRP 93

QY 61 DYDRIRLFENGSLLLSDQLADEGTVEVEISITDDTFTGKTNLTVDVPISRPQVLVA 120

DB 94 DYDRIRLFENGSLLLSDQLADEGTVEVEISITDDTFTGKTNLTVDVPISRPQVLVA 153

QY 121 STTVLEISEAFTLNCSEHGKPSYTWLKDGPPLNDSRMILLSPDQKVLITITVLMEDDD 180

DB 154 STTVLEISEAFTLNCSEHGKPSYTWLKDGPPLNDSRMILLSPDQKVLITITVLMEDDD 213

QY 181 LYSYCWENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLTVCAWKPSKRQKKL 240

DB 214 LYSYCWENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLTVCAWKPSKRQKKL 273

QY 241 EKQNSLEYMDQNDRLKPEADTLPRSGEQRKNPMALYILKDKDSPETENPAPEPSAT 300

DB 274 EKQNSLEYMDQNDRLKPEADTLPRSGEQRKNPMALYILKDKDSPETENPAPEPSAT 333

QY 301 EPGPPGYSVPVPGSRSPGLPIRSARYPRSPARSPATGRTHSSPPRAPSPPGRSRASR 360

DB 334 EPGPPGYSVPVPGSRSPGLPIRSARYPRSPARSPATGRTHSSPPRAPSPPGRSRASR 393

QY 361 TLRTAGVHIIREQDEAGPVEISA 383

DB 394 TLRTAGVHIIREQDEAGPVEISA 416

RESULT 3

ABG75377

ID ABG75377 standard; protein; 416 AA.

XX AC ABG75377;

XX DT 22-APR-2004 (first entry)

XX DE Human INSP052 complete protein.

XX KW INSP052; human; cell proliferation; autoimmune disease; inflammation;
 KW cardiovascular disease; neurological disease; psychiatric disease;
 KW developmental disease; metabolic disorder; infection;
 KW immunoglobulin domain-containing cell surface recognition molecule.

```
OS Homo sapiens.
XX WO2003093316-A2.
XX 13-NOV-2003.
XX 30-APR-2003; 2003WO-GB001851.
XX 30-APR-2002; 2002GB-00009884.
XX (ARES-) ARES TRADING SA.
XX Davids AR, Fagan RJ, Phelps CB, Power C;
XX WPI; 2003-903655/82.
XX N-PSDB; ACH01275.
XX New INSP052 polypeptides and nucleic acids, useful in diagnosing and
XX treating cell proliferative, autoimmune/inflammatory, cardiovascular,
XX neurological, psychiatric, developmental, genetic or metabolic disorder.
XX Claim 1; Page 67; Opp; English.
XX The present invention provides the protein and coding sequences of a
XX novel human immunoglobulin domain-containing cell surface recognition
XX molecule known as INSP052. The polypeptide is useful as immunoglobulin
XX domain-containing cell surface recognition molecule. The sequences may
XX also be used in therapy or diagnosing a disease or in the manufacture of
XX a medicament for treating a disease. The disease is a cell proliferative,
XX autoimmune/inflammatory, cardiovascular, neurological, psychiatric,
XX developmental, genetic or metabolic disorder, an infection or other
XX pathological condition. The polypeptides and nucleic acids are essential
XX to the structural integrity and homeostatic functioning of most tissues.
XX The present sequence is a polypeptide shown in the invention
XX Sequence 416 AA;
XX Query Match 100.0%; Score 1962; DB 7; Length 416;
XX Best Local Similarity 100.0%; Pred. No. 3e-134;
XX Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VNITSPVRLIHGTGKSAALLSVQYSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 60
Db 34 VNITSPVRLIHGTGKSAALLSVQYSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 93
QY 61 DYDRIRLRFENGSLLLSDQLADEGTYEVEISITDDTFTGKTNLTVDVPISRPQVLVA 120
Db 94 DYDRIRLRFENGSLLLSDQLADEGTYEVEISITDDTFTGKTNLTVDVPISRPQVLVA 153
QY 121 STTVLELSEAFTLNCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLTTITRVLMEDD 180
Db 154 STTVLELSEAFTLNCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLTTITRVLMEDD 213
QY 181 LYSWVENPISQGRSLPVKITYRRSSLYIILSTGGIFLLVTLVTVCAKWPSSKQKQL 240
Db 214 LYSWVENPISQGRSLPVKITYRRSSLYIILSTGGIFLLVTLVTVCAKWPSSKQKQL 273
QY 241 EKQNSLEYMDQNDRLKPEADTLPRSGEQERKNPMALYILKDKOSPETEENPAPEPRSAT 300
Db 274 EKQNSLEYMDQNDRLKPEADTLPRSGEQERKNPMALYILKDKOSPETEENPAPEPRSAT 333
QY 301 EPGPGYSVPAVPCRSCLPTRSARRYPSPARSPTATGRTHSSPPRAPSPPGRSRSASR 360
Db 334 EPGPGYSVPAVPCRSCLPTRSARRYPSPARSPTATGRTHSSPPRAPSPPGRSRSASR 393
QY 361 TLRTAGVHIIREQDEAGPVEISA 383
Db 394 TLRTAGVHIIREQDEAGPVEISA 416
RESULT 4
ADO47892
ID ADO47892 standard; protein; 416 AA.
```

```
XX ADO47892;
XX 15-JUL-2004 (first entry)
XX Human protein SEQ ID NO:9.
XX human; virucide; anti-HIV; cytostatic; antinflammatory; antiallergic;
XX immunosuppressive; antiarteriosclerotic; hypotensive; osteopathic;
XX antianaemic; neuroprotective; nootropic; antiparkinsonian; antiasthmatic;
XX haemostatic; antidiabetic; cardiant; HIV; viral infection; cancer;
XX inflammation; allergy; graft rejection; atherosclerosis; hypertension;
XX osteoporosis; anaemia; Alzheimer's disease; Parkinson's disease; asthma;
XX diabetes; myocardial infarction; haemophilia.
XX Homo sapiens.
XX WO2004007672-A2.
XX 22-JAN-2004.
XX 09-JUL-2003; 2003WO-US021703.
XX 12-JUL-2002; 2002US-0395402P.
XX (NUVE-) NUVELO INC.
XX Rupp F, Wang J, Zhou P, Wehrman T, Wang ZW, Tang YT;
XX WPI; 2004-122914/12.
XX N-PSDB; ADO47891.
XX New isolated polypeptides and polynucleotides useful in diagnostics,
XX forensics, in preventing or treating diseases such as HIV and cancer, and
XX as drug targets.
XX Claim 10; SEQ ID NO 9; 205pp; English.
XX The invention relates to novel isolated polynucleotides and polypeptides
XX encoded by them. Also included are mutants or variants of the
XX polynucleotides and polypeptides. A polypeptide of the invention has
XX virucide, anti-HIV, cytostatic, antinflammatory, antiallergic,
XX immunosuppressive, antiarteriosclerotic, hypotensive, osteopathic,
XX antianaemic, neuroprotective, nootropic, antiparkinsonian, antiasthmatic,
XX haemostatic, antidiabetic, and cardiant activity. The composition and
XX methods are useful in diagnostics, forensics, gene or chromosome mapping,
XX identification of mutations responsible for genetic disorders or other
XX traits, in assessing biodiversity, or in producing many other types of
XX data and products dependent on DNA and amino acid sequences. They may
XX also be used in preventing or treating diseases (e.g. HIV and other viral
XX infections, cancer, inflammation, allergies, graft rejection,
XX atherosclerosis, hypertension, osteoporosis, anaemia, Alzheimer's
XX disease, Parkinson's disease, asthma, diabetes, myocardial infarction or
XX haemophilia). They may also be used as targets in drug screening. The
XX present sequence represents a polypeptide of the invention.
XX Sequence 416 AA;
XX Query Match 100.0%; Score 1962; DB 8; Length 416;
XX Best Local Similarity 100.0%; Pred. No. 3e-134;
XX Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VNITSPVRLIHGTGKSAALLSVQYSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 60
Db 34 VNITSPVRLIHGTGKSAALLSVQYSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 93
QY 61 DYDRIRLRFENGSLLLSDQLADEGTYEVEISITDDTFTGKTNLTVDVPISRPQVLVA 120
Db 94 DYDRIRLRFENGSLLLSDQLADEGTYEVEISITDDTFTGKTNLTVDVPISRPQVLVA 153
QY 121 STTVLELSEAFTLNCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLTTITRVLMEDD 180
Db 154 STTVLELSEAFTLNCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLTTITRVLMEDD 213
```

QY	181	LYSCWVENPISQGRSLPVKITVYRRSLYIILSTGGIFLLVTLVTVACWKPSKRQKKL	240
DB	214	LYSCWVENPISQGRSLPVKITVYRRSLYIILSTGGIFLLVTLVTVACWKPSKRQKKL	273
QY	241	EKQNSLEYMDQNDRLKPEADTLPRSGEQERKNPMALYILKDKSPETENPAPEPRSAT	300
DB	274	EKQNSLEYMDQNDRLKPEADTLPRSGEQERKNPMALYILKDKSPETENPAPEPRSAT	333
QY	301	EPGPGYSVSPAVPGRSPGLPIRSARYPRSPARSPATGRTHSSPPRAPSPGSRASR	360
DB	334	EPGPGYSVSPAVPGRSPGLPIRSARYPRSPARSPATGRTHSSPPRAPSPGSRASR	393
QY	361	TLRTAGVHIIREQDEAGPVEISA	383
DB	394	TLRTAGVHIIREQDEAGPVEISA	416
RESULT 5			
ID	ADS11056	standard; protein; 416 AA.	
XX	AC	ADS11056;	
XX	DT	16-DEC-2004 (first entry)	
XX	DE	Human therapeutic protein - SEQ ID 1293.	
XX	KW	antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;	
XX	KW	inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;	
XX	KW	aplastic anaemia; cancer; wound healing; gene therapy.	
XX	OS	Homo sapiens.	
XX	PN	WO2004080148-A2.	
XX	PD	23-SEP-2004.	
XX	PF	30-SEP-2003; 2003WO-US030720.	
XX	PR	02-OCT-2002; 2002US-0416186P.	
XX	PA	(NUVE-) NUVELO INC.	
PI	PI	Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;	
PI	PI	Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;	
XX	DR	WPI; 2004-668857/65.	
DR	DR	N-PSDB; ADS10372.	
XX	PT	New polynucleotide, useful in preparing a composition for diagnosing or	
PT	PT	treating inflammatory, neurodegenerative or stem cell disorders, e.g.,	
PT	PT	aplastic anemia or cancer for promoting wound healing.	
XX	PS	Claim 20; SEQ ID NO 1293; 718pp; English.	
XX	CC	The invention relates to a novel isolated polynucleotide and the encoded	
CC	CC	polypeptide. The molecules of the invention demonstrate antiinflammatory,	
CC	CC	neuroprotective, antianaemic, cytostatic and vulnerary activities and may	
CC	CC	be useful in preparing a composition for diagnosing or treating	
CC	CC	inflammatory, haematopoietic, immune, neurodegenerative or stem cell	
CC	CC	disorders, such as aplastic anaemia or cancer, as well as for promoting	
CC	CC	wound healing. The molecules may also be utilised during gene therapy	
CC	CC	procedures. The current sequence is that of a human therapeutic protein	
CC	CC	of the invention. The current sequence is not shown explicitly within the	
CC	CC	specification but can be accessed from the WIPO web-site.	
XX	SQ	Sequence 416 AA;	
Query Match 100.0%; Score 1962; DB 8; Length 416;			
Best Local Similarity 100.0%; Pred. No. 3e-134;			
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

QY	1	VNITSPVRLIHGTGKSALLSVQYSTSSDRPVWKQLKRPVTVVQSIGTEVIGTLRP	60
DB	34	VNITSPVRLIHGTGKSALLSVQYSTSSDRPVWKQLKRPVTVVQSIGTEVIGTLRP	93
QY	61	DYRDRIRLFENGSLLLSDQLADEGTYVEIISITDDTFTGKTIINLTVDVPISRPQVLVA	120
DB	94	DYRDRIRLFENGSLLLSDQLADEGTYVEIISITDDTFTGKTIINLTVDVPISRPQVLVA	153
QY	121	STTVLELSAFTLNCSHENGTKPSYTWLKDGPLLNDSRMLLSPDQKVLTITRVLMEDDD	180
DB	154	STTVLELSAFTLNCSHENGTKPSYTWLKDGPLLNDSRMLLSPDQKVLTITRVLMEDDD	213
QY	181	LYSCWVENPISQGRSLPVKITVYRRSLYIILSTGGIFLLVTLVTVACWKPSKRQKKL	240
DB	214	LYSCWVENPISQGRSLPVKITVYRRSLYIILSTGGIFLLVTLVTVACWKPSKRQKKL	273
QY	241	EKQNSLEYMDQNDRLKPEADTLPRSGEQERKNPMALYILKDKSPETENPAPEPRSAT	300
DB	274	EKQNSLEYMDQNDRLKPEADTLPRSGEQERKNPMALYILKDKSPETENPAPEPRSAT	333
QY	301	EPGPGYSVSPAVPGRSPGLPIRSARYPRSPARSPATGRTHSSPPRAPSPGSRASR	360
DB	334	EPGPGYSVSPAVPGRSPGLPIRSARYPRSPARSPATGRTHSSPPRAPSPGSRASR	393
QY	361	TLRTAGVHIIREQDEAGPVEISA	383
DB	394	TLRTAGVHIIREQDEAGPVEISA	416
RESULT 6			
ID	ABG75378	standard; protein; 418 AA.	
XX	AC	ABG75378;	
XX	DT	22-APR-2004 (first entry)	
XX	DE	Murine-INSP052 complete protein.	
XX	KW	INSP052; human; cell proliferation; autoimmune disease; inflammation;	
XX	KW	cardiovascular disease; neurological disease; psychiatric disease;	
XX	KW	developmental disease; metabolic disorder; infection;	
XX	KW	immunoglobulin domain-containing cell surface recognition molecule.	
XX	OS	Mus sp.	
XX	PN	WO2003093316-A2.	
XX	PD	13-NOV-2003.	
XX	PF	30-APR-2003; 2003WO-GB001851.	
XX	PR	30-APR-2002; 2002GB-00009884.	
XX	PA	(ARES-) ARES TRADING SA.	
XX	PI	Davids AR, Fagan RJ, Phelps CB, Power C;	
XX	DR	WPI; 2003-903655/82.	
XX	DR	N-PSDB; ACH01276.	
XX	PT	New INSP052 polypeptides and nucleic acids, useful in diagnosing and	
XX	PT	treating cell proliferative, autoimmune/inflammatory, cardiovascular,	
XX	PT	neurological, psychiatric, developmental, genetic or metabolic disorder.	
XX	PS	Example 1; Page 68; Opp; English.	
XX	CC	The present invention provides the protein and coding sequences of a	
XX	CC	novel human immunoglobulin domain-containing cell surface recognition	
XX	CC	molecule known as INSP052. The polypeptide is useful as immunoglobulin	
XX	CC	domain-containing cell surface recognition molecule. The sequences may	
XX	CC	also be used in therapy or diagnosing a disease or in the manufacture of	
XX	CC	a medicament for treating a disease. The disease is a cell proliferative,	

CC autoimmune/inflammatory, cardiovascular, neurological, psychiatric,
CC developmental, genetic or metabolic disorder, an infection or other
CC pathological condition. The polypeptides and nucleic acids are essential
CC to the structural integrity and homeostatic functioning of most tissues.
XX The present sequence is a polypeptide shown in the invention
SQ Sequence 418 AA;

Query Match 94.3%; Score 1850; DB 7; Length 418;
Best Local Similarity 94.5%; Pred. No. 4.2e-126;
Matches 364; Conservative 9; Mismatches 10; Indels 2; Gaps 1;
QY 1 VNITSPVRLIHGTGKALLSVQYSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 60
DB 34 VNITSPVRLIHGTGKALLSVQYSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 93
QY 61 DYDRIRLRFENGSLLSLDQLADEGTYEVEISITDDTFTGKTNLTVDPISRPQVLVA 120
DB 94 DYDRIRLRFENGSLLSLDQLADEGTYEVEISITDDTFTGKTNLTVDPISRPQVLVA 153
QY 121 STTVLELSEAFNLCSHENGKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDDD 180
DB 154 STTVLELSEAFNLCSHENGKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDDD 213
QY 181 LYSCMVENPISQGRSLPVKITVYRRSSLIYILSTGGIFLLVTLVTVCAKWPSPK--RKQK 238
DB 214 LYSCMVENPISQGRSLPVKITVYRRSSLIYILSTGGIFLLVTLVTVCAKWPSPKSRKKR 273
QY 239 KLEKNSLEYMDQNDRLKPEADTLPRSGEQRKNPMALYILKDKSPETENPAPEPRS 298
DB 274 KLEKNSLEYMDQNDRLKPEADTLPRSGEQRKNPMALYILKDKSPEDENPAPEPRS 333
QY 299 ATEPGPGYSVPVPGSPGLPIRSARYPRSPARSATGRTHTSPRPAPSSPGRSRA 358
DB 334 TTEPGPGYSVPVPGSPGLPIRSARYPRSPARSATGRTHTSPRPAPSSPGRSRS 393
QY 359 SRTLRTAGVHIIRQDEAGPVEISA 383
DB 394 SRSLETAGVQRIREQDESGVEISA 418

RESULT 7
ADQ65357
ID ADQ65357 standard; protein; 367 AA.
XX ADQ65357;
AC ADQ65357;
DT 07-OCT-2004 (first entry)
XX Novel human protein sequence #330.
DE
XX osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
KW gene therapy; diagnostic marker; morbid state; osteoporosis;
KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
KW cancer.
XX Homo sapiens.
OS
XX EPI440981-A2.
FN
XX 28-JUL-2004.
PD
XX 21-JAN-2004; 2004EP-00001196.
PF
XX 21-JAN-2003; 2003JP-00102206.
PR
XX 09-MAY-2003; 2003JP-00131392.
PR
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
PA
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Iehii S;
PI Yamamoto J, Isono Y, Nagai K, Irie R;
XX WPI; 2004-535376/52.
DR

DR N-PSDB; ADQ63169.
XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX Claim 1; SEQ ID NO 2518; 2449pp; English.
PS

CC The invention relates to 2495 novel polynucleotides (I) and their encoded
CC polypeptides, sequences hybridizing to these nucleotides, sequences
CC encoding partial polypeptides and sequences having 70% or 90% identity to
CC the nucleotide and protein sequences. The nucleotides and polypeptides
CC are useful as diagnostic markers or therapeutic target for the diseases
CC or morbid states. They are also useful for treating osteoporosis,
CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
CC dementia and various cancers. This sequence corresponds to a protein
CC sequence of the invention.

SQ Sequence 367 AA;

Query Match 67.2%; Score 1318.5; DB 8; Length 367;
Best Local Similarity 83.2%; Pred. No. 1.7e-87;
Matches 272; Conservative 12; Mismatches 26; Indels 17; Gaps 4;
QY 1 VNITSPVRLIHGTGKALLSVQYSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 60
DB 34 VNITSPVRLIHGTGKALLSVQYSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 93
QY 61 DYDRIRLRFENGSLLSLDQLADEGTYEVEISITDDTFTGKTNLTVDPISRPQVLVA 120
DB 94 DYDRIRLRFENGSLLSLDQLADEGTYEVEISITDDTFTGKTNLTVDPISRPQVLVA 153
QY 121 STTVLELSEAFNLCSHENGKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDDD 180
DB 154 STTVLELSEAFNLCSHENGKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDDD 213
QY 181 LYSCMVENPISQGRSLPVKITVYRRSSLIYILSTGGIFLLVTLVTVCAKWPSPKSRKK 240
DB 214 LYSCMVENPISQGRSLPVKITVYRRSSLIYILSTGGIFLLVTLVTVCAKWPSPKSRKK 273
QY 241 EKQNSLEYMDQNDRLKPEADTLPRSGEQRKNPMALYI-----LKDKSPETEE 290
DB 274 EKQNSLEYMDQNDRLKPEGE-LPAT-----QSPIPSTIRSVGCWEKAEKLGKENSAGT 327
QY 291 NPAPEPRS-ATEPGPGYSVPVPGSP 316
DB 328 LPSDLGASKGKEPEPASLASHSLPRR 354

RESULT 8
AAE14784
ID AAE14784 standard; protein; 298 AA.
XX AAE14784;
AC AAE14784;
DT 30-OCT-2002 (first entry)
XX Human immunoglobulin superfamily protein (IGSFP)-4.
DE
XX Human; immunoglobulin superfamily protein-4; IGSFP-4; asthma;
KW immune system disorder; acquired immune deficiency syndrome; AIDS;
KW atherosclerosis; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; developmental disorder; renal tubular acidosis;
KW anaemia; muscle disorder; cardiomyopathy; myocarditis; cancer;
KW cell proliferative disorder; arteriosclerosis; hepatitis.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Key 1..33
FT Peptide /label= Signal_peptide
FT Protein 34..298
FT /note= "Mature IGSFP-4"
FT Region 43..231

Db 1 VNITSPVRLHGTGKSGALLSVQYSSSTSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 60
 Qy 61 DYDRIRLFPENGSLLSDLQADGTYEVEISITDDTFTGKTNLTVDVPISRPQVLVA 120
 Db 61 DYDRIRLFPENGSLLSDLQADGTYEVEISITDDTFTGKTNLTVDVPISRPQVLVA 120
 Qy 121 STTVLESEAFTLNCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLTTITRVLMEDDDD 180
 Db 121 STTVLESEAFTLNCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLTTITRVLMEDDDD 180
 Qy 181 LYSCHWENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLTVTCACWKPSKR 235
 Db 181 LYSCHWENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLTVTCACWKPSKR 235

RESULT 10

ID ADO47887 standard; protein; 270 AA.

XX ADO47887;

XX 15-JUL-2004 (first entry)

XX Human protein SEQ ID NO:4.

XX human; virucide; anti-HIV; cytostatic; antiinflammatory; antiallergic;
 XX immunosuppressive; antiarteriosclerotic; hypotensive; osteopathic;
 XX antianaemic; neuroprotective; nootropic; antiparkinsonian; antiasthmatic;
 XX haemostatic; antidiabetic; cardiant; HIV; viral infection; cancer;
 XX inflammation; allergy; graft rejection; atherosclerosis; hypertension;
 XX osteoporosis; anaemia; Alzheimer's disease; Parkinson's disease; asthma;
 XX diabetes; myocardial infarction; haemophilia.

XX Homo sapiens.

XX WO2004007672-A2.

XX 22-JAN-2004.

XX 09-JUL-2003; 2003WO-US021703.

XX 12-JUL-2002; 2002US-0395402P.

XX (NUVE-) NUVELO INC.

XX Rupp F, Wang J, Zhou P, Wehrman T, Wang ZW, Tang YT;

XX WPI; 2004-122914/12.

XX N-PSDB; ADO47886.

XX New isolated polypeptides and polynucleotides useful in diagnostics, PT
 forensic, in preventing or treating diseases such as HIV and cancer, and
 as drug targets.

XX Claim 10; SEQ ID NO 4; 205pp; English.

XX The invention relates to novel isolated polynucleotides and polypeptides
 CC encoded by them. Also included are mutants or variants of the
 CC polynucleotides and polypeptides. A polypeptide of the invention has
 CC virucide, anti-HIV, cytostatic, antiinflammatory, antiallergic,
 CC immunosuppressive, antiarteriosclerotic, hypotensive, osteopathic,
 CC antianaemic, neuroprotective, nootropic, antiparkinsonian, antiasthmatic,
 CC haemostatic, antidiabetic, and cardiant activity. The composition and
 CC methods are useful in diagnostics, forensics, gene or chromosome mapping,
 CC identification of mutations responsible for genetic disorders or other
 CC traits, in assessing biodiversity, or in producing many other types of
 CC data and products dependent on DNA and amino acid sequences. They may
 CC also be used in preventing or treating diseases (e.g. HIV and other viral
 CC infections, cancer, inflammation, allergies, graft rejection,
 CC atherosclerosis, hypertension, osteoporosis, anaemia, Alzheimer's
 CC disease, Parkinson's disease, asthma, diabetes, myocardial infarction or
 CC haemophilia). They may also be used as targets in drug screening. The
 CC present sequence represents a polypeptide of the invention.

XX SQ Sequence 270 AA;

Query Match 60.8%; Score 1192; DB 8; Length 270;
 Best Local Similarity 100.0%; Pred. No. 1.8e-78;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNITSPVRLHGTGKSGALLSVQYSSSTSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 60
 Db 34 VNITSPVRLHGTGKSGALLSVQYSSSTSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 93
 Qy 61 DYDRIRLFPENGSLLSDLQADGTYEVEISITDDTFTGKTNLTVDVPISRPQVLVA 120
 Db 94 DYDRIRLFPENGSLLSDLQADGTYEVEISITDDTFTGKTNLTVDVPISRPQVLVA 153
 Qy 121 STTVLESEAFTLNCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLTTITRVLMEDDDD 180
 Db 154 STTVLESEAFTLNCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLTTITRVLMEDDDD 213
 Qy 181 LYSCHWENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLTVTCACWKPSKR 235
 Db 214 LYSCHWENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLTVTCACWKPSKR 268

RESULT 11

ID ADS11055

XX ADS11055 standard; protein; 270 AA.

XX ADS11055;

XX 16-DEC-2004 (first entry)

XX Human therapeutic protein - SEQ ID 1292.

XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
 XX inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
 XX aplastic anaemia; cancer; wound healing; gene therapy.

XX Homo sapiens.

XX WO2004080148-A2.

XX 23-SEP-2004.

XX 30-SEP-2003; 2003WO-US030720.

XX 02-OCT-2002; 2002US-0416186P.

XX (NUVE-) NUVELO INC.

XX Tang YT, Asundi V, Ren F, Zhang J, Zhang J, Wehrman T, Wang Z, Ma Y;
 PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;

XX WPI; 2004-668857/65.

XX N-PSDB; ADS10371.

XX New polynucleotide, useful in preparing a composition for diagnosing or
 PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
 PT aplastic anaemia or cancer for promoting wound healing.

XX Claim 20; SEQ ID NO 1292; 718pp; English.

XX The invention relates to a novel isolated polynucleotide and the encoded
 CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
 CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
 CC be useful in preparing a composition for diagnosing or treating
 CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
 CC disorders, such as aplastic anaemia or cancer, as well as for promoting
 CC wound healing. The molecules may also be utilised during gene therapy
 CC procedures. The current sequence is that of a human therapeutic protein
 CC of the invention. The current sequence is not shown explicitly within the
 CC specification but can be accessed from the WIPO web-site.

SQ Sequence 270 AA;
Query Match 60.8%; Score 1192; DB 8; Length 270;
Best Local Similarity 100.0%; Pred. No. 1.8e-78;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VNITSPVRLIHGTGKSGALLSVQYSSSTSDRPVVKWQKRDKPVTVVQSIGTGVIGTLRP 60
DB 34 VNITSPVRLIHGTGKSGALLSVQYSSSTSDRPVVKWQKRDKPVTVVQSIGTGVIGTLRP 93
QY 61 DYDRIRLRFNGSLLSDQLADEGTYEVEISITDDTFTGTEKTNLTFVDVPISRPQVLVA 120
DB 94 DYDRIRLRFNGSLLSDQLADEGTYEVEISITDDTFTGTEKTNLTFVDVPISRPQVLVA 153
QY 121 STTVLELSEAFNLCSHENGTKPSYTWLKDGPILLNDSRMLLSPDQKVLITITRVLMBDD 180
DB 154 STTVLELSEAFNLCSHENGTKPSYTWLKDGPILLNDSRMLLSPDQKVLITITRVLMBDD 213
QY 181 LYSWVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVACWKPSKR 235
DB 214 LYSWVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVACWKPSKR 268
RESULT 12
AAE26421
ID AAE26421 standard; protein; 224 AA.
AC AAE26421;
XX
XX
DT 13-DEC-2002 (first entry)
XX
XX
DE Human transmembrane protein (TMP)-7 protein.
XX
XX
KW Human; transmembrane protein; TMP-7; developmental disorder; epilepsy;
KW prostaticitis; infertility; neurological disorder; Alzheimer's disease;
KW anaemia; stroke; cardiovascular disorder; hypertension; atherosclerosis;
KW gastrointestinal disorder; anorexia; Crohn's disease; lipid metabolism;
KW hypercholesterolaemia; hyperlipidaemia; cell proliferative disorder;
KW psoriasis; autoimmune disorder; acquired immune deficiency syndrome;
KW AIDS; cancer; gout; Grave's disease; transgenic; transgenic animal;
KW gene therapy; antiinfertility; anticonvulsant; hypotensive; nootropic;
KW neuroprotective; cerebroprotective; antiinflammatory; cytostatic;
KW antithyroid.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Domain 51..71
FT /note= "Transmembrane domain"
XX
XX
FN WO200234783-A2.
XX
XX
PD 02-MAY-2002.
XX
XX
PP 26-OCT-2001; 2001WO-US049670.
XX
XX
PR 27-OCT-2000; 2000US-0244017P.
PR 22-NOV-2000; 2000US-0252855P.
PR 07-DEC-2000; 2000US-0251825P.
PR 12-DEC-2000; 2000US-0255085P.
XX
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
XX
PI Warren BA, Xu Y, Yue H, Batra S, Burford N, Gandhi AR, Walia NK;
PI Arvizu C, Tang YT, Lu DAM, Duggan BM, Baughn MR, Lee EA, Khan FA;
PI Nguyen DB, Azimzai Y, Yao MG, Lal PG, Thangavelu K, Ramkumar J;
PI Tran B, Ding L, Au-Young J;
DR WPI; 2002-463354/49.
DR N-PSDB; AAD44098.
XX
XX
PT Novel human transmembrane proteins and polynucleotides useful for
diagnosing, treating or preventing infertility, anemia, hypertension,

PT anorexia, hypercholesterolemia, cancer, gout, Grave's disease.
XX
PS Claim 62; Page 132-133; 163pp; English.
XX
CC The present invention relates to novel human transmembrane proteins (TMP)
CC and polynucleotides encoding such proteins. Sequences of the invention
CC are useful for treating diseases or conditions associated with abnormal
CC expression of TMP such as disorders of reproduction (e.g. infertility,
CC prostaticitis), developmental (e.g. anaemia, epilepsy), gastrointestinal
CC (e.g. anorexia, Crohn's disease), neurological (e.g. Alzheimer's disease,
CC stroke), lipid metabolism (e.g. hypercholesterolaemia, hyperlipidaemia),
CC cardiovascular (e.g. atherosclerosis, hypertension), cell proliferative
CC (e.g. cancer, psoriasis) and autoimmune disorders (e.g. acquired immune
CC deficiency syndrome (AIDS), gout, Grave's disease). They are useful for
CC creating knockout humanised animals or transgenic animals to model human
CC disease. Sequences of the invention are also used in gene therapy. The
XX present sequence is TMP-7 protein
SQ Sequence 224 AA;
Query Match 59.0%; Score 1157; DB 5; Length 224;
Best Local Similarity 100.0%; Pred. No. 4.9e-76;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 160 MLLSPDQKVLITITRVLMBDDLLYSWVENPISQGRSLPVKITVYRRSSLYIILSTGGIFL 219
DB 1 MLLSPDQKVLITITRVLMBDDLLYSWVENPISQGRSLPVKITVYRRSSLYIILSTGGIFL 60
QY 220 LVTLVTVACWKPSKRQKLEKQNSLEYMDQNDRLKPEADTLPRSGEQRKNPMALYI 279
DB 61 LVTLVTVACWKPSKRQKLEKQNSLEYMDQNDRLKPEADTLPRSGEQRKNPMALYI 120
QY 280 LKDKDSPETEENPAPRSPATEPSPGYSVSPVPGRSGPLPIRSARRYPSPARSPATG 339
DB 121 LKDKDSPETEENPAPRSPATEPSPGYSVSPVPGRSGPLPIRSARRYPSPARSPATG 180
QY 340 RTHSSPPRAPSSPGRSRASRTLTAGVHIIRQDEAGPVEISA 383
DB 181 RTHSSPPRAPSSPGRSRASRTLTAGVHIIRQDEAGPVEISA 224
RESULT 13
ABG75380
ID ABG75380 standard; protein; 246 AA.
XX
XX
AC ABG75380;
XX
DT 22-APR-2004 (first entry)
XX
XX
DE INSP052 extracellular domain protein.
XX
KW INSP052; human; cell proliferation; autoimmune disease; inflammation;
KW cardiovascular disease; neurological disease; psychiatric disease;
KW developmental disease; metabolic disorder; infection;
KW immunoglobulin domain-containing cell surface recognition molecule.
XX
OS Unidentified.
FN WO2003093316-A2.
XX
XX
PD 13-NOV-2003.
XX
XX
PP 30-APR-2003; 2003WO-GB001851.
XX
XX
PR 30-APR-2002; 2002GB-00009884.
XX
XX
PA (ARES-) ARES TRADING SA.
XX
XX
PI Davids AR, Fagan RJ, Phelps CB, Power C;
XX
XX
DR WPI; 2003-903655/82.
DR N-PSDB; ACH01279.
XX
XX

PT New INSP052 polypeptides and nucleic acids, useful in diagnosing and
PT treating cell proliferative, autoimmune/inflammatory, cardiovascular,
XX neurological, psychiatric, developmental, genetic or metabolic disorder.
XX Claim 1; Fig 7; Opp; English.

XX The present invention provides the protein and coding sequences of a
CC novel human immunoglobulin domain-containing cell surface recognition
CC molecule known as INSP052. The polypeptide is useful as immunoglobulin
CC domain-containing cell surface recognition molecule. The sequences may
CC also be used in therapy or diagnosing a disease or in the manufacture of
CC a medicament for treating a disease. The disease is a cell proliferative,
CC autoimmune/inflammatory, cardiovascular, neurological, psychiatric,
CC pathological condition. The polypeptides and nucleic acids are essential
CC to the structural integrity and homeostatic functioning of most tissues.
CC The present sequence is a polypeptide shown in the invention

XX SQ Sequence 246 AA;

Query Match 53.3%; Score 1045; DB 7; Length 246;
Best Local Similarity 100.0%; Pred. No. 7.7e-68;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNITSPVRLIHGTGKSAALLSVQSSSTSDRPVVKWQLKRDKPVTVQSIGTEVIGTLRP 60
Db 34 VNITSPVRLIHGTGKSAALLSVQSSSTSDRPVVKWQLKRDKPVTVQSIGTEVIGTLRP 93

Qy 61 DYDRIRLFFENGSLLSLDLQADGTYVEISITDDTFTGKTKINTLVDPISRPQVLVA 120
Db 94 DYDRIRLFFENGSLLSLDLQADGTYVEISITDDTFTGKTKINTLVDPISRPQVLVA 153

Qy 121 STTVLELSEAFTLNCSHENGTKPSYTWLKDGPILLNDSRMLLSPDQKVLITITRVLMEDDD 180
Db 154 STTVLELSEAFTLNCSHENGTKPSYTWLKDGPILLNDSRMLLSPDQKVLITITRVLMEDDD 213

Qy 181 LYSCWVENPISQGRSLPVKITVYRRSS 207
Db 214 LYSCWVENPISQGRSLPVKITVYRRSS 240

RESULT 14
ID ADM87341 standard; protein; 256 AA.

XX ADM87341;

XX 03-JUN-2004 (first entry)

XX Human protein SEQ ID NO:434.

XX respiratory; cytostatic; antiarthritic; antiinflammatory;
KW gastrointestinal; antibacterial; immunosuppressive; antidiabetic;
KW antirheumatic; gene therapy; molecular weight marker; chromosome marker;
KW chromosome tag; genetic fingerprinting; nutritional supplement; cancer;
KW inflammatory condition; arthritis; inflammatory bowel disease;
KW Crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1;
KW graft versus host disease; human.

XX Homo sapiens.

XX WO2004009834-A2.

XX 29-JAN-2004.

XX 19-JUL-2002; 2002WO-US022858.

XX 21-JUL-2001; 2001US-0306971P.

XX 28-MAR-2002; 2002US-00112944.

XX (NUVE-) NUVELO INC.

XX Tang YT, Yang Y, Weng G, Zhang J, Ren F, Xue A, Wang J;

PI Wehrman T, Ghosh MJ, Wang D, Zhao QA, Wang Z;
XX WPI: 2004-143291/14.
DR N-PSDB; ADM87097.

XX New isolated polynucleotides and polypeptides, useful for treating, e.g.
PT cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease,
PT Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
PT versus host disease.

PS Claim 20; SEQ ID NO 434; 591pp; English.

XX The present invention describes an isolated polynucleotide (I): (a)
CC comprising a nucleotide sequence selected from SEQ ID NO:1-244; or (b)
CC which encodes a polypeptide with biological activity, where the
CC polynucleotide hybridises to (I) under stringent hybridisation conditions
CC or has greater than 99% sequence identity with (I). (I) has respiratory,
CC cytosolic, antiarthritic, antiinflammatory, antidiabetic and antirheumatic
CC activities, and can be used in gene therapy. (I) can be used for
CC generating polynucleotides encoding chimeric or fusion proteins and
CC heterologous protein sequences. The polynucleotides can be used to
CC express recombinant protein for analysis, characterisation or therapeutic
CC use; as markers for tissues in which the corresponding protein is
CC preferentially expressed; as molecular weight markers on gels; as
CC chromosome markers or tags to identify chromosomes or to map related gene
CC positions; to compare with endogenous DNA sequences in patients to
CC identify potential genetic disorders; as probes to hybridise and discover
CC genes, related DNA sequences; as a source of information to derive PCR
CC primers for genetic fingerprinting; as a probe to subtract-out known
CC sequences in the process of discovering other novel polynucleotides; for
CC selecting and making oligomers for attachment to a gene chip or other
CC support, including for examination of expression patterns; to raise anti-
CC protein antibodies using DNA immunisation techniques; and as an antigen
CC to raise anti-DNA antibodies or elicit another immune response. The
CC polynucleotides and polypeptides can also be used as nutritional sources
CC or supplements, e.g. as a protein or amino acid supplement, as a carbon
CC source, as a nitrogen source or as a source of carbohydrates. The
CC polynucleotides and polypeptides can also be used to treat cancer. The
CC compositions are useful for promoting better or faster closure of non-
CC healing wounds, for the generation and regeneration of tissues, for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues, and conditions resulting from
CC systemic cytokine damage. The compositions can also be used to treat
CC inflammatory conditions (e.g. arthritis, inflammatory bowel disease or
CC Crohn's disease), sepsis, rheumatoid arthritis, diabetes mellitus type 1
CC or graft versus host disease. The present sequence represents a novel
CC human polypeptide sequence from the present invention. N.B. The sequences
CC for this patent were obtained from the USPTO web site from an equivalent
CC US patent US20040048249A1.

XX SQ Sequence 256 AA;

Query Match 52.4%; Score 1029; DB 8; Length 256;
Best Local Similarity 96.2%; Pred. No. 1.2e-66;
Matches 203; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VNITSPVRLIHGTGKSAALLSVQSSSTSDRPVVKWQLKRDKPVTVQSIGTEVIGTLRP 60
Db 34 VNITSPVRLIHGTGKSAALLSVQSSSTSDRPVVKWQLKRDKPVTVQSIGTEVIGTLRP 93

Qy 61 DYDRIRLFFENGSLLSLDLQADGTYVEISITDDTFTGKTKINTLVDPISRPQVLVA 120
Db 94 DYDRIRLFFENGSLLSLDLQADGTYVEISITDDTFTGKTKINTLVDPISRPQVLVA 153

Qy 121 STTVLELSEAFTLNCSHENGTKPSYTWLKDGPILLNDSRMLLSPDQKVLITITRVLMEDDD 180
Db 154 STTVLELSEAFTLNCSHENGTKPSYTWLKDGPILLNDSRMLLSPDQKVLITITRVLMEDDD 213

Qy 181 LYSCWVENPISQGRSLPVKITVYRRSSLYII 211

Db 214 LYSCWVENPISQGRSLPVKITVYRRSSLYII 244

Search completed: July 26, 2005, 16:07:36
Job time : 110.756 secs

RESULT 15
AAM24238
ID AAM24238 standard; protein; 256 AA.
XX
AC AAM24238;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST encoded protein SEQ ID NO: 1763.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KW gene therapy; nutrition.
XX
OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002687.
XX
PR 25-JAN-2000; 2000US-00491404.
PR 17-JUL-2000; 2000US-00617746.
PR 03-AUG-2000; 2000US-00631451.
PR 15-SEP-2000; 2000US-00863870.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
DR WPI; 2001-476164/51.
DR N-ESDB; AAH98897.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use.
XX
PS Claim 20; Page 1159-1160; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention
XX
SQ Sequence 256 AA;

Query Match 51.9%; Score 1018; DB 4; Length 256;
Best Local Similarity 96.6%; Pred. No. 7.5e-66;
Matches 201; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VNITSPVRLIHGTGKSMALLSVQYSSSTSSDRPVVKWQLKRDKPTVVQSIGTEVIGTLRP 60
Db |||||
34 VNITSPVRLIHGTGKSMALLSVQYSSSTSSDRPVVKWQLKRDKPTVVQSIGTEVIGTLRP 93
Qy |||||
61 DYDRIRLFPENGSLLLSLQLADEGTVEVEISITDDTFTGKTNLTVDVPISRPQVIVA 120
Db |||||
94 DYDRIRLFPENGSLLLSLQLADEGTVEVEISITDDTFTGKTNLTVDVPISRPQVILGA 153
Qy |||||
121 STTVLELSEAFTLNCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDDD 180
Db |||||
154 STTVLELSEAFTLNCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDDD 213
Qy |||||
181 LYSCHVENPISQGRSLPVKITVYRRSSL 208
Db |||||
214 LYSCHVENPISQGRSLPVKITVYRRSSL 241

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OM protein - protein search, using sw model

Run on: July 26, 2005, 15:54:21 ; Search time 58.6445 Seconds
(without alignments)
1365.166 Million cell updates/sec

Title: US-10-706-691-22
Perfect score: 1045
Sequence: 1 VNITSPVRLHGTGKSGALL.....NPISQGRSLPVKITVRRSS 207

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1045	100.0	237	8	ADO47890 Human mat
2	1045	100.0	246	7	Abg75380 INSP052 e
3	1045	100.0	270	8	ADO47887 Human pro
4	1045	100.0	270	8	ADs11055 Human pro
5	1045	100.0	298	5	AAE14784 Human imm
6	1045	100.0	383	8	ADO47895 Human mat
7	1045	100.0	416	7	ABG75379 Predicted
8	1045	100.0	416	7	ABG75377 Human INS
9	1045	100.0	416	8	ADO47892 Human pro
10	1045	100.0	416	8	ADs11056 Human the
11	1032	98.8	367	8	ADQ65357 Novel hum
12	1029	98.5	418	7	ABG75378 Murine IN
13	1014	97.0	256	4	AAm24238 Human EST
14	1014	97.0	256	8	ADM87341 Human pro
15	1014	97.0	256	8	ADM87787 Human EST
16	1014	97.0	256	8	ADs112269 Human the
17	1014	97.0	256	8	ADs112268 Human the
18	548	52.4	114	7	ABG75371 Human INS
19	484	46.3	188	7	ABG75372 Human INS
20	268	25.6	338	4	AAm78339 Human pro
21	268	25.6	450	2	AAy13398 Amino aci
22	268	25.6	450	3	ADC78632 Human PRO
23	268	25.6	450	4	AAAB80266 Human PRO
24	268	25.6	450	4	AAU12360 Human PRO
25	268	25.6	450	5	AAU81958 Human PRO

26	268	25.6	450	6	ABU71644	Human PRO
27	268	25.6	450	6	ABO17804	Novel hum
28	268	25.6	450	6	ABU71499	Human PRO
29	268	25.6	450	6	ABU81058	Human PRO
30	268	25.6	450	6	ABU71945	Human sec
31	268	25.6	450	6	ABO01828	Novel hum
32	268	25.6	450	6	ABU66758	Human PRO
33	268	25.6	450	6	ABU54401	Human sec
34	268	25.6	450	6	ABO47416	Human sec
35	268	25.6	450	6	ABU59839	Novel sec
36	268	25.6	450	6	ABO25029	Human sec
37	268	25.6	450	6	ABU64553	Human sec
38	268	25.6	450	6	ABU67399	Human sec
39	268	25.6	450	6	ABO14919	Human sec
40	268	25.6	450	6	ABU67034	Human sec
41	268	25.6	450	6	ABU69676	Novel hum
42	268	25.6	450	6	ABO14858	Human sec
43	268	25.6	450	6	ADA45897	Novel hum
44	268	25.6	450	6	ADA76328	Human PRO
45	268	25.6	450	6	ADB29524	Human sec

ALIGNMENTS

RESULT 1
ADO47890
ID ADO47890 standard; protein; 237 AA.

XX ADO47890;

DT 15-JUL-2004 (first entry)

DE Human mature protein SEQ ID NO:7.

XX human; virucide; anti-HIV; cytostatic; antiinflammatory; antiallergic;
KW immunosuppressive; antiarteriosclerotic; hypotensive; osteopathic;
KW antianaemic; neuroprotective; nootropic; antiparkinsonian; antiasthmatic;
KW haemostatic; antidiabetic; cardiant; HIV; viral infection; cancer;
KW inflammation; allergy; graft rejection; atherosclerosis; hypertension;
KW osteoporosis; anaemia; Alzheimer's disease; Parkinson's disease; asthma;
KW diabetes; myocardial infarction; haemophilia.

XX Homo sapiens.

XX WO2004007672-A2.

XX 22-JAN-2004.

XX 09-JUL-2003; 2003WO-US021703.

XX 12-JUL-2002; 2002US-0395402P.

XX (NUVE-) NUVELO INC.

XX Rupp F, Wang J, Zhou P, Wehrman T, Wang ZW, Tang YT;

XX WPI; 2004-122914/12.

XX N-PSDB; ADO47888.

XX New isolated polypeptides and polynucleotides useful in diagnostics, forensics, in preventing or treating diseases such as HIV and cancer, and as drug targets.

XX Claim 10; SEQ ID NO 7; 205pp; English.

XX The invention relates to novel isolated polynucleotides and polypeptides encoded by them. Also included are mutants or variants of the polynucleotides and polypeptides. A polypeptide of the invention has virucide, anti-HIV, cytostatic, antiinflammatory, antiallergic, immunosuppressive, antiarteriosclerotic, hypotensive, osteopathic, antianaemic, neuroprotective, nootropic, antiparkinsonian, antiasthmatic, haemostatic, antidiabetic, and cardiant activity. The composition and

CC methods are useful in diagnostics, forensics, gene or chromosome mapping,
 CC identification of mutations responsible for genetic disorders or other
 CC traits, in assessing biodiversity, or in producing many other types of
 CC data and products dependent on DNA and amino acid sequences. They may
 CC also be used in preventing or treating diseases (e.g. HIV and other viral
 CC infections, cancer, inflammation, allergies, graft rejection,
 CC atherosclerosis, hypertension, osteoporosis, anaemia, Alzheimer's
 CC disease, Parkinson's disease, asthma, diabetes, myocardial infarction or
 CC haemophilia). They may also be used as targets in drug screening. The
 CC present sequence represents a polypeptide of the invention.

XX SQ Sequence 237 AA;

Query Match 100.0%; Score 1045; DB 8; Length 237;
 Best Local Similarity 100.0%; Pred. No. 8.4e-83;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNITSPVRLIHGTGKSGALLSVQSSSTSDRPVVKWQKRDKPTVVVQSIGTEVIGTLRP 60
 Db 1 VNITSPVRLIHGTGKSGALLSVQSSSTSDRPVVKWQKRDKPTVVVQSIGTEVIGTLRP 60
 Qy 61 DYDRIRLRFENGSLLSLDLQADSGTYEVEISITDDTFTGKKTINLTVDVPISRPQVLVA 120
 Db 61 DYDRIRLRFENGSLLSLDLQADSGTYEVEISITDDTFTGKKTINLTVDVPISRPQVLVA 120
 Qy 121 STTVLELSEAFTLNCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDDD 180
 Db 121 STTVLELSEAFTLNCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDDD 180
 Qy 181 LYSWMVENPISQGRSLPVKITVYRRSS 207
 Db 181 LYSWMVENPISQGRSLPVKITVYRRSS 207

RESULT 2

ADBG75380
 ID ABG75380 standard; protein; 246 AA.

XX AC ABG75380;

XX DT 22-APR-2004 (first entry)

XX DE INSP052 extracellular domain protein.

XX KW INSP052; human; cell proliferation; autoimmune disease; inflammation;
 KW cardiovascular disease; neurological disease; psychiatric disease;
 KW developmental disease; metabolic disorder; infection;
 KW immunoglobulin domain-containing cell surface recognition molecule.

XX OS Unidentified.

XX FN WO2003093316-A2.

XX PD 13-NOV-2003.

XX PF 30-APR-2003; 2003WO-GB001851.

XX PR 30-APR-2002; 2002GB-00009884.

XX PA (ARES-) ARES TRADING SA.

XX PI Davids AR, Fagan RJ, Phelps CB, Power C;

XX DR WPI; 2003-903655/82.

XX DR N-PSDB; ACH01279.

XX PT New INSP052 polypeptides and nucleic acids, useful in diagnosing and
 PT treating cell proliferative, autoimmune/inflammatory, cardiovascular,
 PT neurological, psychiatric, developmental, genetic or metabolic disorder.

XX PS Claim 1; Fig 7; Opp; English.

XX CC The present invention provides the protein and coding sequences of a

CC novel human immunoglobulin domain-containing cell surface recognition
 CC molecule known as INSP052. The polypeptide is useful as immunoglobulin
 CC domain-containing cell surface recognition molecule. The sequences may
 CC also be used in therapy or diagnosing a disease or in the manufacture of
 CC a medicament for treating a disease. The disease is a cell proliferative,
 CC autoimmune/inflammatory, cardiovascular, neurological, psychiatric,
 CC developmental, genetic or metabolic disorder, an infection or other
 CC pathological condition. The polypeptides and nucleic acids are essential
 CC to the structural integrity and homeostatic functioning of most tissues.
 CC The present sequence is a polypeptide shown in the invention

XX SQ Sequence 246 AA;

Query Match 100.0%; Score 1045; DB 7; Length 246;
 Best Local Similarity 100.0%; Pred. No. 8.8e-83;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNITSPVRLIHGTGKSGALLSVQSSSTSDRPVVKWQKRDKPTVVVQSIGTEVIGTLRP 60
 Db 34 VNITSPVRLIHGTGKSGALLSVQSSSTSDRPVVKWQKRDKPTVVVQSIGTEVIGTLRP 93
 Qy 61 DYDRIRLRFENGSLLSLDLQADSGTYEVEISITDDTFTGKKTINLTVDVPISRPQVLVA 120
 Db 94 DYDRIRLRFENGSLLSLDLQADSGTYEVEISITDDTFTGKKTINLTVDVPISRPQVLVA 153
 Qy 121 STTVLELSEAFTLNCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDDD 180
 Db 154 STTVLELSEAFTLNCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDDD 213
 Qy 181 LYSWMVENPISQGRSLPVKITVYRRSS 207
 Db 214 LYSWMVENPISQGRSLPVKITVYRRSS 240

RESULT 3

ADO47887

ID ADO47887 standard; protein; 270 AA.

XX AC ADO47887;

XX DT 15-JUL-2004 (first entry)

XX DE Human protein SEQ ID NO:4.

XX KW human; virucide; anti-HIV; cytostatic; antiinflammatory; antiallergic;
 KW immunosuppressive; antiarteriosclerotic; hypotensive; osteopathic;
 KW antianaemic; neuroprotective; nootropic; antiparkinsonian; antiasthmatic;
 KW haemostatic; antidiabetic; cardiant; HIV; viral infection; cancer;
 KW inflammation; allergy; graft rejection; atherosclerosis; hypertension;
 KW osteoporosis; anaemia; Alzheimer's disease; Parkinson's disease; asthma;
 KW diabetes; myocardial infarction; haemophilia.

XX OS Homo sapiens.

XX PN WO2004007672-A2.

XX PD 22-JAN-2004.

XX PF 09-JUL-2003; 2003WO-US021703.

XX PR 12-JUL-2002; 2002US-0395402P.

XX PA (NUVE-) NUVELO INC.

XX PI Rupp F, Wang J, Zhou P, Wehrman T, Wang ZW, Tang YT;

XX DR WPI; 2004-122914/12.

XX DR N-PSDB; ADO47886.

XX PT New isolated polypeptides and polynucleotides useful in diagnostics,
 PT forensics, in preventing or treating diseases such as HIV and cancer, and
 PT as drug targets.

PS Claim 10; SEQ ID NO 4; 205pp; English.

XX The invention relates to novel isolated polynucleotides and polypeptides

CC encoded by them. Also included are mutants or variants of the

CC polynucleotides and polypeptides. A polypeptide of the invention has

CC virucide, anti-HIV, cytostatic, antiinflammatory, antiallergic,

CC immunosuppressive, antiatherosclerotic, hypotensive, osteopathic,

CC antianaemic, neuroprotective, nootropic, antiparkinsonian, antiasthmatic,

CC haemostatic, antidiabetic, and cardiant activity. The composition and

CC methods are useful in diagnostics, forensics, gene or chromosome mapping,

CC identification of mutations responsible for genetic disorders or other

CC traits, in assessing biodiversity, or in producing many other types of

CC data and products dependent on DNA and amino acid sequences. They may

CC also be used in preventing or treating diseases (e.g. HIV and other viral

CC infections, cancer, inflammation, allergies, graft rejection,

CC atherosclerosis, hypertension, osteoporosis, anaemia, Alzheimer's

CC disease, Parkinson's disease, asthma, diabetes, myocardial infarction or

CC haemophilia). They may also be used as targets in drug screening. The

CC present sequence represents a polypeptide of the invention.

XX

SQ Sequence 270 AA;

Query Match 100.0%; Score 1045; DB 8; Length 270;

Best Local Similarity 100.0%; Pred. No. 9.9e-83;

Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNITSPVRLIHGTGKSAALLSVQSSSTSDRPVVKWQKRDKPVTTVQSIGTEVIGTLRP 60

DB 34 VNITSPVRLIHGTGKSAALLSVQSSSTSDRPVVKWQKRDKPVTTVQSIGTEVIGTLRP 93

QY 61 DYRDRIRLFENGSLLLSDQLADEGTYEVEISITDDTFTGKTKINLTVDVPISRPQVLVA 120

DB 94 DYRDRIRLFENGSLLLSDQLADEGTYEVEISITDDTFTGKTKINLTVDVPISRPQVLVA 153

QY 121 STTVLELSEAFTLNCSHENGTKPSYTWLKGKPLNLSRMLLSPDQKVLTTITRVLMEDDD 180

DB 154 STTVLELSEAFTLNCSHENGTKPSYTWLKGKPLNLSRMLLSPDQKVLTTITRVLMEDDD 213

QY 181 LYSWCWENPISQGRSLPKVITVYRRSS 207

DB 214 LYSWCWENPISQGRSLPKVITVYRRSS 240

RESULT 4

ADSI1055

ID ADSI1055 standard; protein; 270 AA.

XX

AC ADSI1055;

XX

DT 16-DEC-2004 (first entry)

XX

DE Human therapeutic protein - SEQ ID 1292.

XX

KW antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;

KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;

KW aplastic anaemia; cancer; wound healing; gene therapy.

XX

OS Homo sapiens.

XX

FN WO2004080148-A2.

XX

PD 23-SEP-2004.

XX

PF 30-SEP-2003; 2003WO-US030720.

XX

PR 02-OCT-2002; 2002US-0416186P.

XX

XX (NUVE-) NUVELO INC.

XX

XX Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;

PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;

XX WPI; 2004-668857/65.

DR

DR N-PSDB; ADS10371.

XX

PT New polynucleotide, useful in preparing a composition for diagnosing or

PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,

PT aplastic anemia or cancer for promoting wound healing.

XX

PS Claim 20; SEQ ID NO 1292; 718pp; English.

XX

CC The invention relates to a novel isolated polynucleotide and the encoded

CC polypeptide. The molecules of the invention demonstrate antiinflammatory,

CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may

CC be useful in preparing a composition for diagnosing or treating

CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell

CC disorders, such as aplastic anaemia or cancer, as well as for promoting

CC wound healing. The molecules may also be utilised during gene therapy

CC procedures. The current sequence is that of a human therapeutic protein

CC of the invention. The current sequence is not shown explicitly within the

CC specification but can be accessed from the WIFO web-site.

XX

SQ Sequence 270 AA;

Query Match 100.0%; Score 1045; DB 8; Length 270;

Best Local Similarity 100.0%; Pred. No. 9.9e-83;

Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNITSPVRLIHGTGKSAALLSVQSSSTSDRPVVKWQKRDKPVTTVQSIGTEVIGTLRP 60

DB 34 VNITSPVRLIHGTGKSAALLSVQSSSTSDRPVVKWQKRDKPVTTVQSIGTEVIGTLRP 93

QY 61 DYRDRIRLFENGSLLLSDQLADEGTYEVEISITDDTFTGKTKINLTVDVPISRPQVLVA 120

DB 94 DYRDRIRLFENGSLLLSDQLADEGTYEVEISITDDTFTGKTKINLTVDVPISRPQVLVA 153

QY 121 STTVLELSEAFTLNCSHENGTKPSYTWLKGKPLNLSRMLLSPDQKVLTTITRVLMEDDD 180

DB 154 STTVLELSEAFTLNCSHENGTKPSYTWLKGKPLNLSRMLLSPDQKVLTTITRVLMEDDD 213

QY 181 LYSWCWENPISQGRSLPKVITVYRRSS 207

DB 214 LYSWCWENPISQGRSLPKVITVYRRSS 240

RESULT 5

AAE14784

ID AAE14784 standard; protein; 298 AA.

XX

AC AAE14784;

XX

DT 30-OCT-2002 (first entry)

XX

DE Human immunoglobulin superfamily protein (IGSFP)-4.

XX

KW Human; immunoglobulin superfamily protein-4; IGSFP-4; asthma;

KW immune system disorder; acquired immune deficiency syndrome; AIDS;

KW atherosclerosis; neurological disorder; Alzheimer's disease;

KW Parkinson's disease; developmental disorder; renal tubular acidosis;

KW anaemia; muscle disorder; cardiomyopathy; myocarditis; cancer;

KW cell proliferative disorder; arteriosclerosis; hepatitis.

XX

OS Homo sapiens.

XX

FN

PH Location/Qualifiers

FT Peptide 1..33

FT /label= Signal_peptide

FT Protein 34..298

FT /note= "Mature IGSFP-4"

FT Region 43..231

FT /note= "Antigen precursor signal immunoglobulin fold

FT glycoprotein T cell surface transmembrane"

FT Domain 48..120

FT /label= Immunoglobulin_domain

FT Domain 161..219

FT /label= Immunoglobulin_domain

FT	Domain	243...263 /label= Transmembrane_domain
FX	WO200240671-A2.	
FX	23-MAY-2002.	
FX	15-NOV-2001; 2001WO-US044974.	
FX	16-NOV-2000; 2000US-0249645P.	
FX	(INCY-) INCYTE GENOMICS INC.	
FX	Baughn MR, Lu DAM, Yue H, Elliott VS, Thangavelu K, Ramkumar J;	
FX	Lu Y, Lo TP, Gururajan R, Gandhi AR, Arvizu C, Yao MG;	
FX	WPI; 2002-519384/55.	
FX	N-PSDB; AAD36780.	
FX	Novel human immunoglobulin superfamily polypeptide, useful in diagnosis,	
FX	prevention or treatment of immune system, neurological, developmental,	
FX	muscle and cell proliferative disorders.	
FX	Claim 1; Page 109-110; 122pp; English.	
FX	The present sequence is human immunoglobulin superfamily protein (IGSFP)-	
FX	4. The IGSFP polypeptide and polynucleotide are useful for diagnosing,	
FX	treating or preventing disorders associated with aberrant expression of	
FX	IGSFP e.g. immune system disorders (e.g. acquired immune deficiency	
FX	syndrome (AIDS), asthma, atherosclerosis, psoriasis, uveitis),	
FX	neurological disorders (e.g. Alzheimer's disease, Huntington's disease,	
FX	dementia, Parkinson's disease), developmental disorders (e.g. renal	
FX	tubular acidosis, epilepsy, anaemia), muscle disorders (e.g.	
FX	cardiomyopathy, myocarditis), or cell proliferative disorders (e.g.	
FX	arteriosclerosis, cirrhosis, hepatitis, and cancer). The polypeptide and	
FX	polynucleotide are also useful for assessing the effects of exogenous	
FX	compounds on their expression. The polypeptide is useful in drug	
FX	screening techniques, to analyse the proteome of a tissue or cell type,	
FX	as elements on a microarray. The polynucleotide is useful for creating	
FX	knock-in humanised animals or transgenic animals to model human diseases,	
FX	in somatic or germline gene therapy, to generate a transcript image of a	
FX	tissue or cell type, for detecting differences in the chromosomal	
FX	location due to translocation, inversion among normal, carrier or	
FX	affected individuals, and as hybridisation probes for mapping naturally	
FX	occurring genomic sequences	
FX	Sequence 298 AA;	
FX	Query Match 100.0%; Score 1045; DB 5; Length 298;	
FX	Best Local Similarity 100.0%; Pred. No. 1.1e-82;	
FX	Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 VNITSPVRLIHGTGKSAALLSVQYSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 60	
Db	34 VNITSPVRLIHGTGKSAALLSVQYSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 93	
Qy	61 DYDRIRLRFENGSLLLSDQLADEGTVEVEISITDDTFTGKKTINLTVDVPISRPQVLVA 120	
Db	94 DYDRIRLRFENGSLLLSDQLADEGTVEVEISITDDTFTGKKTINLTVDVPISRPQVLVA 153	
Qy	121 STTVLELSEAFTLNCSHENGTKPSYTWLKDCKPILLNDSRMLLSPDQKVLITITRVLMEDDD 180	
Db	154 STTVLELSEAFTLNCSHENGTKPSYTWLKDCKPILLNDSRMLLSPDQKVLITITRVLMEDDD 213	
Qy	181 LYSWCVENPISQGRSLPVKITVYRRSS 207	
Db	214 LYSWCVENPISQGRSLPVKITVYRRSS 240	
FX	RESULT 6	
FX	ADO47895	
FX	ID ADO47895 standard; protein; 383 AA.	
FX		
AC	ADO47895;	
XX	15-JUL-2004 (first entry)	
DT	Human mature protein SEQ ID NO:12.	
XX	human; virucide; anti-HIV; cytostatic; antiinflammatory; antiallergic;	
XX	immunosuppressive; antiarteriosclerotic; hypotensive; osteopathic;	
XX	antianaemic; neuroprotective; nootropic; antiparkinsonian; antiasthmatic;	
XX	haemostatic; antidiabetic; cardiant; HIV; viral infection; cancer;	
XX	inflammation; allergy; graft rejection; atherosclerosis; hypertension;	
XX	osteoporosis; anaemia; Alzheimer's disease; Parkinson's disease; asthma;	
XX	diabetes; myocardial infarction; haemophilia.	
XX	Homo sapiens.	
OS	WO2004007672-A2.	
XX	22-JAN-2004.	
XX	09-JUL-2003; 2003WO-US021703.	
FX	12-JUL-2002; 2002US-0395402P.	
XX	(NUVE-) NUVELO INC.	
XX	Rupp F, Wang J, Zhou P, Wehrman T, Wang ZW, Tang YT;	
XX	WPI; 2004-122914/12.	
XX	N-PSDB; ADO47893.	
XX	New isolated polypeptides and polynucleotides useful in diagnostics,	
XX	forensics, in preventing or treating diseases such as HIV and cancer, and	
XX	as drug targets.	
XX	Claim 10; SEQ ID NO 12; 205pp; English.	
XX	The invention relates to novel isolated polynucleotides and polypeptides	
XX	encoded by them. Also included are mutants or variants of the	
XX	polynucleotides and polypeptides. A polypeptide of the invention has	
XX	virucide, anti-HIV, cytostatic, antiinflammatory, antiallergic,	
XX	immunosuppressive, antiarteriosclerotic, hypotensive, osteopathic,	
XX	antianaemic, neuroprotective, nootropic, antiparkinsonian, antiasthmatic,	
XX	haemostatic, antidiabetic, and cardiant activity. The composition and	
XX	methods are useful in diagnostics, forensics, gene or chromosome mapping,	
XX	identification of mutations responsible for genetic disorders or other	
XX	traits, in assessing biodiversity, or in producing many other types of	
XX	data and products dependent on DNA and amino acid sequences. They may	
XX	also be used in preventing or treating diseases (e.g. HIV and other viral	
XX	infections, cancer, inflammation, allergies, graft rejection,	
XX	atherosclerosis, hypertension, osteoporosis, anaemia, Alzheimer's	
XX	disease, Parkinson's disease, asthma, diabetes, myocardial infarction or	
XX	haemophilia). They may also be used as targets in drug screening. The	
XX	present sequence represents a polypeptide of the invention.	
XX	Sequence 383 AA;	
XX	Query Match 100.0%; Score 1045; DB 8; Length 383;	
XX	Best Local Similarity 100.0%; Pred. No. 1.6e-82;	
XX	Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 VNITSPVRLIHGTGKSAALLSVQYSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 60	
Db	1 VNITSPVRLIHGTGKSAALLSVQYSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 60	
Qy	61 DYDRIRLRFENGSLLLSDQLADEGTVEVEISITDDTFTGKKTINLTVDVPISRPQVLVA 120	
Db	61 DYDRIRLRFENGSLLLSDQLADEGTVEVEISITDDTFTGKKTINLTVDVPISRPQVLVA 120	
Qy	121 STTVLELSEAFTLNCSHENGTKPSYTWLKDCKPILLNDSRMLLSPDQKVLITITRVLMEDDD 180	
Db	121 STTVLELSEAFTLNCSHENGTKPSYTWLKDCKPILLNDSRMLLSPDQKVLITITRVLMEDDD 180	


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QY 181 LYSWENPISQGRSLPVKITVYRRSS 207
Db 214 LYSWENPISQGRSLPVKITVYRRSS 240

RESULT 9
AD047892
ID ADO47892 standard; protein; 416 AA.
XX
AC ADO47892;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human protein SEQ ID NO:9.
XX
KW human; virucide; anti-HIV; cytostatic; antiinflammatory; antiallergic;
KW immunosuppressive; antiarteriosclerotic; hypotensive; osteopathic;
KW antianaemic; neuroprotective; nootropic; antiparkinsonian; antiasthmatic;
KW haemostatic; antidiabetic; cardiant; HIV; viral infection; cancer;
KW inflammation; allergy; graft rejection; atherosclerosis; hypertension;
KW osteoporosis; anaemia; Alzheimer's disease; Parkinson's disease; asthma;
KW diabetes; myocardial infarction; haemophilia.
XX
OS Homo sapiens.
XX
XX WO2004007672-A2.
XX
XX 22-JAN-2004.
XX
XX 09-JUL-2003; 2003WO-US021703.
XX
XX 12-JUL-2002; 2002US-0395402P.
XX
XX (NUVE-) NUVELO INC.
XX
XX Rupp F, Wang J, Zhou P, Wehrman T, Wang ZW, Tang YT;
XX WPI: 2004-122914/12.
XX
XX N-PSDB; ADO47891.
XX
XX New isolated polypeptides and polynucleotides useful in diagnostics,
XX forensics, in preventing or treating diseases such as HIV and cancer, and
XX as drug targets.
XX
XX Claim 10; SEQ ID NO 9; 205pp; English.
XX
XX The invention relates to novel isolated polynucleotides and polypeptides
XX encoded by them. Also included are mutants or variants of the
XX polynucleotides and polypeptides. A polypeptide of the invention has
XX virucide, anti-HIV, cytostatic, antiinflammatory, antiallergic,
XX immunosuppressive, antiarteriosclerotic, hypotensive, osteopathic,
XX antianaemic, neuroprotective, nootropic, antiparkinsonian, antiasthmatic,
XX haemostatic, antidiabetic, and cardiant activity. The composition and
XX methods are useful in diagnostics, forensics, gene or chromosome mapping,
XX identification of mutations responsible for genetic disorders or other
XX traits, in assessing biodiversity, or in producing many other types of
XX data and products dependent on DNA and amino acid sequences. They may
XX also be used in preventing or treating diseases (e.g. HIV and other viral
XX infections, cancer, inflammation, allergies, graft rejection,
XX atherosclerosis, hypertension, osteoporosis, anaemia, Alzheimer's
XX disease, Parkinson's disease, asthma, diabetes, myocardial infarction or
XX haemophilia). They may also be used as targets in drug screening. The
XX present sequence represents a polypeptide of the invention.
XX
XX Sequence 416 AA;
XX
XX Query Match 100.0%; Score 1045; DB 8; Length 416;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-82;
XX Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 VNITSPVRLIHGTGKSAALLSVQSSSTSDRPVVKQLKRDKPVTVVQSIGTEVIGTLRP 60
Db 34 VNITSPVRLIHGTGKSAALLSVQSSSTSDRPVVKQLKRDKPVTVVQSIGTEVIGTLRP 93

us-10-706-691-22.rag
QY 61 DYDRIRLPENGSLLSLDLQADGTYVEVEISITDDTFTGKKTINLTVDVIPSRQVLVA 120
Db 94 DYDRIRLPENGSLLSLDLQADGTYVEVEISITDDTFTGKKTINLTVDVIPSRQVLVA 153

RESULT 10
ADSL1056
ID ADSL1056 standard; protein; 416 AA.
XX
AC ADSL1056;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human therapeutic protein - SEQ ID 1293.
XX
XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
XX inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
XX aplastic anaemia; cancer; wound healing; gene therapy.
XX
XX Homo sapiens.
XX
XX WO2004080148-A2.
XX
XX 23-SEP-2004.
XX
XX 30-SEP-2003; 2003WO-US030720.
XX
XX 02-OCT-2002; 2002US-0416186P.
XX
XX (NUVE-) NUVELO INC.
XX
XX Tang YT, Asundi V, Ren F, Zhang J, Zhang J, Wehrman T, Wang Z, Ma Y;
XX Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX WPI: 2004-668857/65.
XX
XX N-PSDB; ADS10372.
XX
XX New polynucleotide, useful in preparing a composition for diagnosing or
XX treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
XX aplastic anemia or cancer for promoting wound healing.
XX
XX Claim 20; SEQ ID NO 1293; 718pp; English.
XX
XX The invention relates to a novel isolated polynucleotide and the encoded
XX polypeptide. The molecules of the invention demonstrate antiinflammatory,
XX neuroprotective, antianaemic, cytostatic and vulnerary activities and may
XX be useful in preparing a composition for diagnosing or treating
XX inflammatory, haematopoietic, immune, neurodegenerative or stem cell
XX disorders, such as aplastic anaemia or cancer, as well as for promoting
XX wound healing. The molecules may also be utilised during gene therapy
XX procedures. The current sequence is that of a human therapeutic protein
XX of the invention. The current sequence is not shown explicitly within the
XX specification but can be accessed from the WIPO web-site.
XX
XX Sequence 416 AA;
XX
XX Query Match 100.0%; Score 1045; DB 8; Length 416;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-82;
XX Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 VNITSPVRLIHGTGKSAALLSVQSSSTSDRPVVKQLKRDKPVTVVQSIGTEVIGTLRP 60
Db 34 VNITSPVRLIHGTGKSAALLSVQSSSTSDRPVVKQLKRDKPVTVVQSIGTEVIGTLRP 93

```

Db	94	DSRDRIRLFENGSLLLSDLOLADSGTVEVEISITDDTFTGKTNLNTVDVPSRPQVLVA	153
Qy	121	STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLNDSRMLLSPDQKVTITRVLMEDDD	180
Db	154	STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLNDSRMLLSPDQKVTITRVLMEDDD	213
Qy	181	LYSCWENPISQGRSLPVKITVYRRSS	207
Db	214	LYSCWENPISQGRSLPVKITVYRRSS	240

RESULT 12	
ABG75378	
ID	ABG75378 standard; protein; 418 AA.
XX	
XX	AC ABG75378;
XX	
XX	22-APR-2004 (first entry)
XX	
DE	Murine INSP052 complete protein.
XX	
XX	INSP052; human; cell proliferation; autoimmune disease; inflammation;
KW	cardiovascular disease; neurological disease; psychiatric disease;
KW	developmental disease; metabolic disorder; infection;
KW	immunoglobulin domain-containing cell surface recognition molecule.
XX	
XX	Mus sp.
OS	
XX	WO2003093316-A2.
PN	
XX	
PD	13-NOV-2003.
XX	
XX	
PF	30-APR-2003; 2003WO-GB001851.
XX	
XX	
PR	30-APR-2002; 2002GB-00009884.
XX	
XX	(ARES-) ARES TRADING SA.
PA	

XX	WPI; 2003-903655/82.
XX	N-PSDB; ACH01276.
XX	
XX	New INSP052 polypeptides and nucleic acids, useful in diagnosing and
XX	treating cell proliferative, autoimmune/inflammatory, cardiovascular,
XX	neurological, psychiatric, developmental, genetic or metabolic disorder.
XX	
XX	Example 1; Page 68; Opp; English.
XX	
XX	The present invention provides the protein and coding sequences of a
XX	novel human immunoglobulin domain-containing cell surface recognition
XX	molecule known as INSP052. The polypeptide is useful as immunoglobulin
XX	domain-containing cell surface recognition molecule. The sequences may
XX	also be used in therapy or diagnosing a disease or in the manufacture of
XX	a medicament for treating a disease. The disease is a cell proliferative,
XX	autoimmune/inflammatory, cardiovascular, neurological, psychiatric,
XX	developmental, genetic or metabolic disorder, an infection or other
XX	pathological condition. The polypeptides and nucleic acids are essential
XX	to the structural integrity and homeostatic functioning of most tissues.
XX	The present sequence is a polypeptide shown in the invention

SQ		Sequence 418 AA;	
Query Match	98.5%;	Score 1029; DB 7;	Length 418;
Best Local Similarity	98.6%;	Pred. No.	4.3e-81;
Matches 204; Conservative	2; Mismatches	1; Indels	0; Gaps 0

QY	60
Db	93
QY	120

Db 94 DYDRIRLFENGSLLSLDQLADEGTYEVEISITDDTFTGKTNLTVDVPISRQVLVA 153
Qy 121 STTVLESEAFNLCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDEDD 180
Db 154 STTVLESEAFNLCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDEDD 213
Qy 181 LYSVMENPISQGRSLPVKITVYRRSS 207
Db 214 LYSVVENPISQGRSLPVKITVYRRSS 240

RESULT 13
AAM24238
ID AAM24238 standard; protein; 256 AA.
XX
AC AAM24238;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST encoded protein SEQ ID NO: 1763.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KW gene therapy; nutrition.
XX
OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002687.
XX
PR 25-JAN-2000; 2000US-00491404.
PR 17-JUL-2000; 2000US-00617746.
PR 03-AUG-2000; 2000US-00631451.
PR 15-SEP-2000; 2000US-00663870.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
XX WPI; 2001-476164/51.
DR N-PSDB; AAH98897.
XX
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
XX antibodies and research use.
XX
PS Claim 20; Page 1159-1160; 1275pp; English.
XX
XX The present invention provides the protein and coding sequences of novel
XX proteins from a variety of organisms, including human, dog, cat, horse,
XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
XX urchin and tomato. These were derived from expressed sequence tags (ESTs)
XX from the organism of interest. They can be used in diagnostics,
XX forensics, gene mapping, identification of mutations, to assess
XX biodiversity and for nutritional purposes. The present sequence is a
XX protein of the invention
XX
SQ Sequence 256 AA;
Query Match 97.0%; Score 1014; DB 4; Length 256;
Best Local Similarity 96.6%; Pred. No. 4.6e-80;
Matches 200; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VNITSPVRLHGTGKSALLSVQYSSSTSSDRPVVKWQLKRDKPTVWQSIGTEVIGTLRP 60
Db 34 VNITSPVRLHGTGKSALLSVQYSSSTSSDRPVVKWQLKRDKPTVWQSIGTEVIGTLRP 93
Qy 61 DYDRIRLFENGSLLSLDQLADEGTYEVEISITDDTFTGKTNLTVDVPISRQVLVA 120

Db 94 DYDRIRLFENGSLLSLDQLADEGTYEVEISITDDTFTGKTNLTVDVPISRQVLGA 153
Qy 121 STTVLESEAFNLCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDEDD 180
Db 154 STTVLESEAFNLCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDEDD 213
Qy 181 LYSVMENPISQGRSLPVKITVYRRSS 207
Db 214 LYSVVENPISQGRSLPVKITVYRRSS 240

RESULT 14
ADM87341
ID ADM87341 standard; protein; 256 AA.
XX
AC ADM87341;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human protein SEQ ID NO:434.
XX
KW respiratory; cytostatic; antiarthritic; antiinflammatory;
KW gastrointestinal; antibacterial; immunosuppressive; antidiabetic;
KW antirheumatic; gene therapy; molecular weight marker; chromosome marker;
KW chromosome tag; genetic fingerprinting; nutritional supplement; cancer;
KW inflammatory condition; arthritis; inflammatory bowel disease;
KW Crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1;
KW graft versus host disease; human.
XX
XX Homo sapiens.
XX
PN WO2004009834-A2.
XX
PD 29-JAN-2004.
XX
PF 19-JUL-2002; 2002WO-US022858.
PR 21-JUL-2001; 2001US-0306971P.
PR 28-MAR-2002; 2002US-00112944.
XX
XX (NUVE-) NUVELO INC.
XX
PI Tang YT, Yang Y, Weng G, Zhang J, Ren F, Xue A, Wang J;
PI Wehrman T, Ghosh MJ, Wang D, Zhao QA, Wang Z;
XX
XX WPI; 2004-143291/14.
DR N-PSDB; ADM87097.
XX
XX New isolated polynucleotides and polypeptides, useful for treating, e.g.
XX cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease,
XX Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
XX versus host disease.
XX
XX Claim 20; SEQ ID NO 434; 591pp; English.
XX
XX The present invention describes an isolated polynucleotide (I): (a)
XX comprising a nucleotide sequence selected from SEQ ID NO:1-244; or (b)
XX which encodes a polypeptide with biological activity, where the
XX polynucleotide hybridises to (I) under stringent hybridisation conditions
XX or has greater than 99% sequence identity with (I). (I) has respiratory,
XX cytostatic, antiarthritic, antiinflammatory, gastrointestinal,
XX antibacterial, immunosuppressive, antidiabetic and antirheumatic
XX activities, and can be used in gene therapy. (I) can be used for
XX generating polynucleotides encoding chimeric or fusion proteins and
XX heterologous protein sequences. The polynucleotides can be used to
XX express recombinant protein for analysis, characterisation or therapeutic
XX use; as markers for tissues in which the corresponding protein is
XX preferentially expressed; as molecular weight markers on gels; as
XX chromosome markers or tags to identify chromosomes or to map related gene
XX positions; to compare with endogenous DNA sequences in patients to
XX identify potential genetic disorders; as probes to hybridise and discover
XX genes, related DNA sequences; as a source of information to derive PCR

CC primers for genetic fingerprinting; as a probe to subtract-out known
 CC sequences in the process of discovering other novel polynucleotides; for
 CC selecting and making oligomers for attachment to a gene chip or other
 CC support, including for examination of expression patterns; to raise anti-
 CC protein antibodies using DNA immunisation techniques; and as an antigen
 CC to raise anti-DNA antibodies or elicit another immune response. The
 CC polynucleotides and polypeptides can also be used as nutritional sources
 CC or supplements, e.g. as a protein or amino acid supplement, as a carbon
 CC source, as a nitrogen source or as a source of carbohydrates. The
 CC polynucleotides and polypeptides can also be used to treat cancer. The
 CC compositions are useful for promoting better or faster closure of non-
 CC healing wounds, for the generation and regeneration of tissues, for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, and conditions resulting from
 CC systemic cytokine damage. The compositions can also be used to treat
 CC inflammatory conditions (e.g. arthritis, inflammatory bowel disease or
 CC Crohn's disease), sepsis, rheumatoid arthritis, diabetes mellitus type 1
 CC or graft versus host disease. The present sequence represents a novel
 CC human polypeptide sequence from the present invention. N.B. The sequences
 CC for this patent were obtained from the USPTO web site from an equivalent
 CC US patent US20040048249A1.

XX SQ Sequence 256 AA;

Query Match 97.0%; Score 1014; DB 8; Length 256;
 Best Local Similarity 96.6%; Pred. No. 4.6e-80;
 Matches 200; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 VNITSPVRLHGTGKSAALLSVQSSSTSDRPVVKWQLKRDKPVTVQSIGTEVIGTLRP 60
 DB |||||
 QY 34 VNITSPVRLHGTGKSAALLSVQSSSTSDRPVVKWQLKRDKPVTVQSIGTEVIGTLRP 93
 DB |||||
 QY 61 DYDRIRLRFENGSLLSLDQLADEGTVEVEISITDDTFTGKTLNLTVDVPISRPQVLVA 120
 DB |||||
 QY 94 DYDRIRLRFENGSLLSLDQLADEGTVEVEISITDDTFTGKTLNLTVDVPISRPQVLVA 153
 DB |||||
 QY 121 STTVLELSEAFTLNCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITTRVLMEDDD 180
 DB |||||
 QY 154 STTVLELSEAFTLNCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITTRVLMEDDD 213
 DB |||||
 QY 181 LYSQWENPISQGRSLPVKTIYRRSS 207
 DB |||||
 QY 214 LDCVVENPISQGRSLPVKTIYRRSS 240
 DB |||||

RESULT 15

ADM87787
 ID ADM87787 standard; protein; 256 AA.

XX AC ADM87787;

XX DT 03-JUN-2004 (first entry)

XX DE Human EST derived amino acid sequence SEQ ID NO:880.

XX KW respiratory; cytostatic; antiarthritis; antiinflammatory;
 KW gastrointestinal; antibacterial; immunosuppressive; antidiabetic;
 KW anirrhematic; gene therapy; molecular weight marker; chromosome marker;
 KW chromosome tag; genetic fingerprinting; nutritional supplement; cancer;
 KW inflammatory condition; arthritis; inflammatory bowel disease;
 KW Crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1;
 KW graft versus host disease; human; expressed sequence tag; EST.

XX OS Homo sapiens.

XX FN WO2004009834-A2.

XX PD 29-JAN-2004.

XX PF 19-JUL-2002; 2002WO-US022858.

XX PR 21-JUL-2001; 2001US-0306971P.

XX PR 28-MAR-2002; 2002US-00112944.

XX (NUVE-) NUVELO INC.

XX Tang YT, Yang Y, Weng G, Zhang J, Ren F, Xue A, Wang J;

XX Wehrman T, Ghosh M, Wang D, Zhao QA, Wang Z;

XX WPI; 2004-143291/14.

XX N-PSDB; ADM87569.

XX New isolated polynucleotides and polypeptides, useful for treating, e.g.
 XX cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease,
 XX Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
 XX versus host disease.

XX Example 2; SEQ ID NO 880; 591pp; English.

XX The present invention describes an isolated polynucleotide (I): (a)
 XX comprising a nucleotide sequence selected from SEQ ID NO:1-244; or (b)
 XX which encodes a polypeptide with biological activity, where the
 XX polynucleotide hybridises to (I) under stringent hybridisation conditions
 XX or has greater than 98% sequence identity with (I). (I) has respiratory,
 XX cytostatic, antiarthritis, antiinflammatory, gastrointestinal, anti-
 XX bacterial, immunosuppressive, antidiabetic and antineoplastic
 XX activities, and can be used in gene therapy. (I) can be used for
 XX generating polynucleotides encoding chimeric or fusion proteins and
 XX heterologous protein sequences. The polynucleotides can be used to
 XX express recombinant protein for analysis, characterisation or therapeutic
 XX use; as markers for tissues in which the corresponding protein is
 XX preferentially expressed; as molecular weight markers on gels; as
 XX chromosome markers or tags to identify chromosomes or to map related gene
 XX positions; to compare with endogenous DNA sequences in patients to
 XX identify potential genetic disorders; as probes to hybridise and discover
 XX genes, related DNA sequences; as a source of information to derive PCR
 XX primers for genetic fingerprinting; as a probe to subtract-out known
 XX sequences in the process of discovering other novel polynucleotides; for
 XX selecting and making oligomers for attachment to a gene chip or other
 XX support, including for examination of expression patterns; to raise anti-
 XX protein antibodies using DNA immunisation techniques; and as an antigen
 XX to raise anti-DNA antibodies or elicit another immune response. The
 XX polynucleotides and polypeptides can also be used as nutritional sources
 XX or supplements, e.g. as a protein or amino acid supplement, as a carbon
 XX source, as a nitrogen source or as a source of carbohydrates. The
 XX polynucleotides and polypeptides can also be used to treat cancer. The
 XX compositions are useful for promoting better or faster closure of non-
 XX healing wounds, for the generation and regeneration of tissues, for gut
 XX protection or regeneration and treatment of lung or liver fibrosis,
 XX reperfusion injury in various tissues, and conditions resulting from
 XX systemic cytokine damage. The compositions can also be used to treat
 XX inflammatory conditions (e.g. arthritis, inflammatory bowel disease or
 XX Crohn's disease), sepsis, rheumatoid arthritis, diabetes mellitus type 1
 XX or graft versus host disease. The present sequence represents an
 XX expressed sequence tag (EST) derived amino acid sequence from the present
 XX invention. N.B. The sequences for this patent were obtained from the
 XX USPTO web site from an equivalent US patent US20040048249A1.

XX SQ Sequence 256 AA;

Query Match 97.0%; Score 1014; DB 8; Length 256;

Best Local Similarity 96.6%; Pred. No. 4.6e-80;

Matches 200; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNITSPVRLHGTGKSAALLSVQSSSTSDRPVVKWQLKRDKPVTVQSIGTEVIGTLRP 60

DB |||||

QY 34 VNITSPVRLHGTGKSAALLSVQSSSTSDRPVVKWQLKRDKPVTVQSIGTEVIGTLRP 93

DB |||||

QY 61 DYDRIRLRFENGSLLSLDQLADEGTVEVEISITDDTFTGKTLNLTVDVPISRPQVLVA 120

DB |||||

QY 94 DYDRIRLRFENGSLLSLDQLADEGTVEVEISITDDTFTGKTLNLTVDVPISRPQVLVA 153

DB |||||

QY 121 STTVLELSEAFTLNCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITTRVLMEDDD 180

DB |||||

QY 154 STTVLELSEAFTLNCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITTRVLMEDDD 213

Qy 181 LYSCWENPISQGRSLPVKITVYRRSS 207
Db 214 LYSCWENPISQGRSLPVKITVYRRSS 240

Search completed: July 26, 2005, 16:07:34
Job time : 59.8945 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2005, 15:58:52 ; Search time 15.2841 seconds
(without alignments)
1011.008 Million cell updates/sec

Title: US-10-706-691-22
Perfect score: 1045
Sequence: 1 VNITSPVRLHGTGKSAALL.....NPISQGRSLPVKITVYRRSS 207

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	268	25.6	450	4	US-09-907-794A-320
2	268	25.6	450	4	Sequence 320, App
3	268	25.6	450	4	Sequence 320, App
4	268	25.6	450	4	Sequence 320, App
5	268	25.6	450	4	Sequence 320, App
6	268	25.6	450	4	Sequence 320, App
7	268	25.6	450	4	Sequence 320, App
8	268	25.6	450	4	Sequence 320, App
9	268	25.6	450	4	Sequence 320, App
10	163.5	15.6	826	4	US-09-877-730-16
11	163.5	15.6	904	4	US-09-877-730-6
12	163.5	15.6	907	4	US-09-877-730-20
13	163.5	15.6	985	4	US-09-877-730-10
14	163.5	15.6	991	4	US-09-877-730-12
15	163.5	15.6	1069	4	US-09-877-730-2
16	163.5	15.6	1072	4	US-09-877-730-18
17	163.5	15.6	1150	4	US-09-877-730-8
18	163	15.6	316	4	US-09-397-243D-13
19	161.5	15.5	300	4	US-09-254-465A-10
20	161.5	15.5	300	4	US-09-397-243D-12
21	161.5	15.5	300	4	US-09-953-499-10
22	161	15.4	321	6	5169835-17
23	161	15.4	321	6	5169835-17
24	161	15.4	344	2	US-08-602-725-34
25	159	15.2	248	6	5169835-15
26	159	15.2	248	6	5169835-15
27	159	15.2	365	4	US-09-949-016-7591

Sequence 24, Appl
Sequence 24, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 189, App
Sequence 331, App
Sequence 2, Appl
Sequence 1, Appl
Sequence 189, App

ALIGNMENTS

RESULT 1

US-09-907-794A-320
; Sequence 320, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547


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Query Match      25.6%; Score 268; DB 4; Length 450;
Best Local Similarity 31.9%; Pred. No. 2.2e-18;
Matches 67; Conservative 43; Mismatches 90; Indels 10; Gaps 7;

QY      1 VNITSPVRLHGTGKSAALLSVQYS--STSSDRPVVKWOLKR--DKPVTVVQSIGTEVIG 56
DB      20 LKVTVEHSVTHVGVRGQALYLPVHYGHTPASDIOII-WLFRPHITWPKYLLGSVNKSVVP 78

QY      57 TLRPDYRDIRLF-ENGSLLLSLQLADGTYVEVEISIT-DDTFTGKTNLTNLTVDVPISR 114
DB      79 DL--EYQHKFTWMPNPNASLLINPLQPPDEGNIYVKVNIQNGNGLTSASQKIQTVDVDPVK 136

QY      115 PQVILV-ASTVILELSAFTLNCSHENGTYKPSYTWLXGKGPLLNDNRMLSPDKVLTITR 173
DB      137 PVYQIHPPGAGVEYGVNMTLTCHVEGGTSLAYQMLKNGRPVHTSTSYSPQNNTLHIAP 196

QY      174 VLMEDDDLYSVMVENPISGRSLPVKITVY 203
DB      197 VTKEDIGNYSCLVRNPVSEMSDIINPIIY 226

RESULT 4
US-09-906-700-320
; Sequence 320, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,700
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15

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1 PRIOR APPLICATION NUMBER: PCT/US99/23089
2 PRIOR FILING DATE: 1999-10-05
3 PRIOR APPLICATION NUMBER: PCT/US99/28214
4 PRIOR FILING DATE: 1999-11-29
5 PRIOR APPLICATION NUMBER: PCT/US99/28313
6 PRIOR FILING DATE: 1999-11-30
7 PRIOR APPLICATION NUMBER: PCT/US99/28564
8 PRIOR FILING DATE: 1999-12-02
9 PRIOR APPLICATION NUMBER: PCT/US99/28565
10 PRIOR FILING DATE: 1999-12-02
11 PRIOR APPLICATION NUMBER: PCT/US99/30095
12 PRIOR FILING DATE: 1999-12-16
13 PRIOR APPLICATION NUMBER: PCT/US99/30911
14 PRIOR FILING DATE: 1999-12-20
15 PRIOR APPLICATION NUMBER: PCT/US99/30999
16 PRIOR FILING DATE: 1999-12-20
17 PRIOR APPLICATION NUMBER: PCT/US00/00219
18 PRIOR FILING DATE: 2000-01-05
19 NUMBER OF SEQ ID NOS: 423
20 SEQ ID NO 320
21 LENGTH: 450
22 TYPE: PRT
23 ORGANISM: Homo Sapien
24 US-09-906-700-320

Query Match 25.6%; Score 268; DB 4; Length 450;
Best Local Similarity 31.9%; Pred. No. 2.2e-18;
Matches 67; Conservative 43; Mismatches 90; Indels 10; Gaps 7;
Qy 1 VNITSPVRLIHGTGKSAISVQYS--STSSDRPVVKWQLKR--DKPVTVVQSIGTEVIG 56
Db 20 LKVTVPSTHTVHGQALYLPVHYGHTPASDII--WLFERPHTMPKYLGSVNSVWP 78
Qy 57 TLRPDYRDRIRLF-ENGSLLSLDIQLADEGTYVEISIT-DDTFTGKTNLTVDVPISR 114
Db 79 DL--EYQHKFTMPNPASLLINPLQFPDEGNYIVKVNIOGNTLSASQKIQTVDVDPVK 136
Qy 115 PQVLV-ASTTVLELSEAFNLCSHENGTKPSYTWLKGKPLNDRLMLSPDQKVLITR 173
Db 137 PVQIHPPSGAVEYVGNMILTCHVEGGTRLAYQWLKNGRPVHTSTSYFSFQNTLHIAP 196
Qy 174 VLMEDDDLYSVMENPISQGRSLPVKITVY 203
Db 197 VTKEIDIGNYSCLVRNPVSEMSDIIPIIY 226

RESULT 5
US-09-903-603A-320
; Sequence 320, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.

1 APPLICANT: Tumas, Daniel
2 APPLICANT: Williams, P. Mickey
3 APPLICANT: Wood, William, I.
4 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
5 FILE OF INVENTION: Acids Encoding the Same
6 FILE REFERENCE: GNE.1618P2C12
7 CURRENT APPLICATION NUMBER: US/09/903,603A
8 CURRENT FILING DATE: 2001-07-11
9 PRIOR APPLICATION NUMBER: PCT/US00/04414
10 PRIOR FILING DATE: 2000-02-22
11 PRIOR APPLICATION NUMBER: US 60/143,048
12 PRIOR FILING DATE: 1999-07-07
13 PRIOR APPLICATION NUMBER: US 60/145,698
14 PRIOR FILING DATE: 1999-07-26
15 PRIOR APPLICATION NUMBER: US 60/146,222
16 PRIOR FILING DATE: 1999-07-28
17 PRIOR APPLICATION NUMBER: PCT/US99/20594
18 PRIOR FILING DATE: 1999-09-08
19 PRIOR APPLICATION NUMBER: PCT/US99/20944
20 PRIOR FILING DATE: 1999-09-13
21 PRIOR APPLICATION NUMBER: PCT/US99/21090
22 PRIOR FILING DATE: 1999-09-15
23 PRIOR APPLICATION NUMBER: PCT/US99/21547
24 PRIOR FILING DATE: 1999-09-15
25 PRIOR APPLICATION NUMBER: PCT/US99/23089
26 PRIOR FILING DATE: 1999-10-05
27 PRIOR APPLICATION NUMBER: PCT/US99/28214
28 PRIOR FILING DATE: 1999-11-29
29 PRIOR APPLICATION NUMBER: PCT/US99/28313
30 PRIOR FILING DATE: 1999-11-30
31 PRIOR APPLICATION NUMBER: PCT/US99/28564
32 PRIOR APPLICATION NUMBER: PCT/US99/28565
33 PRIOR FILING DATE: 1999-12-02
34 PRIOR APPLICATION NUMBER: PCT/US99/30095
35 PRIOR FILING DATE: 1999-12-16
36 PRIOR APPLICATION NUMBER: PCT/US99/30911
37 PRIOR FILING DATE: 1999-12-20
38 PRIOR APPLICATION NUMBER: PCT/US99/30999
39 PRIOR FILING DATE: 1999-12-20
40 PRIOR APPLICATION NUMBER: PCT/US00/00219
41 PRIOR FILING DATE: 2000-01-05
42 NUMBER OF SEQ ID NOS: 423
43 SEQ ID NO 320
44 LENGTH: 450
45 TYPE: PRT
46 ORGANISM: Homo Sapien
47 US-09-903-603A-320
Query Match 25.6%; Score 268; DB 4; Length 450;
Best Local Similarity 31.9%; Pred. No. 2.2e-18;
Matches 67; Conservative 43; Mismatches 90; Indels 10; Gaps 7;
Qy 1 VNITSPVRLIHGTGKSAISVQYS--STSSDRPVVKWQLKR--DKPVTVVQSIGTEVIG 56
Db 20 LKVTVPSTHTVHGQALYLPVHYGHTPASDII--WLFERPHTMPKYLGSVNSVWP 78
Qy 57 TLRPDYRDRIRLF-ENGSLLSLDIQLADEGTYVEISIT-DDTFTGKTNLTVDVPISR 114
Db 79 DL--EYQHKFTMPNPASLLINPLQFPDEGNYIVKVNIOGNTLSASQKIQTVDVDPVK 136
Qy 115 PQVLV-ASTTVLELSEAFNLCSHENGTKPSYTWLKGKPLNDRLMLSPDQKVLITR 173
Db 137 PVQIHPPSGAVEYVGNMILTCHVEGGTRLAYQWLKNGRPVHTSTSYFSFQNTLHIAP 196
Qy 174 VLMEDDDLYSVMENPISQGRSLPVKITVY 203
Db 197 VTKEIDIGNYSCLVRNPVSEMSDIIPIIY 226

RESULT 6
US-09-904-920A-320
; Sequence 320, Application US/09904920A


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; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 320
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-909-064-320

Query Match      25.6%; Score 268; DB 4; Length 450;
Best Local Similarity 31.9%; Pred. No. 2.2e-18;
Matches 67; Conservative 43; Mismatches 90; Indels 10; Gaps 7;

Qy 1 VNITSPVRLIHGTGKALLSVQYS--STSSDRPVVKWQLK--DKPVTWVQSIGTEVIG 56
Db 20 LKVTVPSTHTVHGVRGQALYLPVHYGFHTPASDIQII-WLPERPHTMPKYLKGSVNSKSWP 78
Qy 57 TLRPDYDRIRLP-ENGSLLSLDLQADGTYEVEISIT-DDTFTGKTTNLTVDVPIR 114
Db 79 DL--EYQHKFTMPNPASLLINPLQFPDEGNYIVKVNIOGNTLSASQKIQTVDDEPVTK 136
Qy 115 PQVLV-ASTTVLELSEAFNLCSHENGTKPSYTWLKDGPLLNDSRMLLSPDQKVLITR 173
Db 137 PVQIHPPSGAVEYVGNMTLTCHVEGTRLAYQWLKNGRPVHTSSTYSFSPQNTLHIAP 196
Qy 174 VLMEDDDLVSCMVENPISQGRSLPVKITVY 203
Db 197 VTKEDIGNYSCLVRNPVSEMSDIIMPIIY 226

RESULT 8
US-09-905-381A-320
; Sequence 320, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel

Query Match      25.6%; Score 268; DB 4; Length 450;
Best Local Similarity 31.9%; Pred. No. 2.2e-18;
Matches 67; Conservative 43; Mismatches 90; Indels 10; Gaps 7;

Qy 1 VNITSPVRLIHGTGKALLSVQYS--STSSDRPVVKWQLK--DKPVTWVQSIGTEVIG 56
Db 20 LKVTVPSTHTVHGVRGQALYLPVHYGFHTPASDIQII-WLPERPHTMPKYLKGSVNSKSWP 78
Qy 57 TLRPDYDRIRLP-ENGSLLSLDLQADGTYEVEISIT-DDTFTGKTTNLTVDVPIR 114
Db 79 DL--EYQHKFTMPNPASLLINPLQFPDEGNYIVKVNIOGNTLSASQKIQTVDDEPVTK 136
Qy 115 PQVLV-ASTTVLELSEAFNLCSHENGTKPSYTWLKDGPLLNDSRMLLSPDQKVLITR 173
Db 137 PVQIHPPSGAVEYVGNMTLTCHVEGTRLAYQWLKNGRPVHTSSTYSFSPQNTLHIAP 196
Qy 174 VLMEDDDLVSCMVENPISQGRSLPVKITVY 203
Db 197 VTKEDIGNYSCLVRNPVSEMSDIIMPIIY 226

RESULT 9
US-09-906-618-320
; Sequence 320, Application US/09906618
; Patent No. 6828146
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APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Abuin, Alejandro
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
CURRENT APPLICATION NUMBER: US/09/877,730
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,607
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 904
TYPE: PRT
ORGANISM: homo sapiens
US-09-877-730-6

Query Match 15.6%; Score 163.5; DB 4; Length 904;
Best Local Similarity 26.9%; Pred. No. 1.7e-07;
Matches 58; Conservative 34; Mismatches 63; Indels 61; Gaps 11;

Qy 2 NITSPVRLIHGTVGKSALLSVQYSSSTSDRPPVVKWQLKRDKPVTVVQSIGTEVIGTLRPD 61
Db 243 NITTS---LHQTV-----VLECMATGNPKPIISWSRLDHSIDV---FNTRVLG----- 285

Qy 62 YRDRIRLFENGSLLSLDQLADEGTYEVEISITDDTFTGKKTINLTVDVPISRPOVLVAS 121
Db 286 -----NGNLMISDVRLQAHGVVYVCR-----TTPGTRNFT----- 320

Qy 122 TTVL-----ELSAFT-----LNCSEHNGTKPSYTWLKDGPFLNDSRMLLSPDQK 167
Db 321 LTVLAPPSFVEWPESLTPRAGTARFVCAEGIPSPKMSWLKNGRKIHSGRIKMYNSK- 379

Qy 168 VLTITRVLMEDDDLSCMVENPISQGRSLP-VKITV 202
Db 380 -LVINQIIPEDDAIYQCMEN--SQGSILSRALTV 412

RESULT 12
US-09-877-730-20
; Sequence 20, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0189-USA
; CURRENT APPLICATION NUMBER: US/09/877,730
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,607
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 907
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-20

Query Match 15.6%; Score 163.5; DB 4; Length 907;
Best Local Similarity 26.9%; Pred. No. 1.7e-07;
Matches 58; Conservative 34; Mismatches 63; Indels 61; Gaps 11;

Qy 2 NITSPVRLIHGTVGKSALLSVQYSSSTSDRPPVVKWQLKRDKPVTVVQSIGTEVIGTLRPD 61
Db 243 NITTS---LHQTV-----VLECMATGNPKPIISWSRLDHSIDV---FNTRVLG----- 285

Db 165 NITTS---LHQTV-----VLECMATGNPKPIISWSRLDHSIDV---FNTRVLG----- 207
Qy 62 YRDRIRLFENGSLLSLDQLADEGTYEVEISITDDTFTGKKTINLTVDVPISRPOVLVAS 121
Db 208 -----NGNLMISDVRLQAHGVVYVCR-----TTPGTRNFT----- 242

Qy 122 TTVL-----ELSAFT-----LNCSEHNGTKPSYTWLKDGPFLNDSRMLLSPDQK 167
Db 243 LTVLAPPSFVEWPESLTPRAGTARFVCAEGIPSPKMSWLKNGRKIHSGRIKMYNSK- 301

Qy 168 VLTITRVLMEDDDLSCMVENPISQGRSLP-VKITV 202
Db 302 -LVINQIIPEDDAIYQCMEN--SQGSILSRALTV 334

RESULT 13
US-09-877-730-10
; Sequence 10, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0189-USA
; CURRENT APPLICATION NUMBER: US/09/877,730
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,607
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 985
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-10

Query Match 15.6%; Score 163.5; DB 4; Length 985;
Best Local Similarity 26.9%; Pred. No. 1.9e-07;
Matches 58; Conservative 34; Mismatches 63; Indels 61; Gaps 11;

Qy 2 NITSPVRLIHGTVGKSALLSVQYSSSTSDRPPVVKWQLKRDKPVTVVQSIGTEVIGTLRPD 61
Db 243 NITTS---LHQTV-----VLECMATGNPKPIISWSRLDHSIDV---FNTRVLG----- 285

Qy 62 YRDRIRLFENGSLLSLDQLADEGTYEVEISITDDTFTGKKTINLTVDVPISRPOVLVAS 121
Db 286 -----NGNLMISDVRLQAHGVVYVCR-----TTPGTRNFT----- 320

Qy 122 TTVL-----ELSAFT-----LNCSEHNGTKPSYTWLKDGPFLNDSRMLLSPDQK 167
Db 321 LTVLAPPSFVEWPESLTPRAGTARFVCAEGIPSPKMSWLKNGRKIHSGRIKMYNSK- 379

Qy 168 VLTITRVLMEDDDLSCMVENPISQGRSLP-VKITV 202
Db 380 -LVINQIIPEDDAIYQCMEN--SQGSILSRALTV 412

RESULT 14
US-09-877-730-12
; Sequence 12, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian

```

Query Match      15.6%; Score 163.5; DB 4; Length 1069;
Best Local Similarity 26.9%; Pred. No. 2.le-07;
Matches 58; Conservative 34; Mismatches 63; Indels 61; Gaps 11;

QY      2 NITSPVRLIHGTGKSAALLSVQVSSSTSDSPVVKQLKRDKPVTVVQSICTEVIIGTLRPD 61
      ||| : ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      243 NITTS---LHQTV-----VLECMATGNPKPIISWSRLDHKSIDV---FNTRVLG----- 285

QY      62 YRDRILFENGSLLLSDQLADGTEVEVEISITDFTTGKTLNLVVDVPIRPOVLVAS 121
      ||| : ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      286 -----NGNLMISDRLQHGAGVVCRA-----TTPGTRNFT-----VAMAT 320

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 16:01:42 ; Search time 52.996 Seconds
(without alignments)
1519.387 Million cell updates/sec

Title: US-10-706-691-22
Perfect score: 1045
Sequence: 1 VNITSPVRLIHGTGKALL.....NPISQGRSLPVKITVYRRSS 207

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 38892284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1045	100.0	207	16	US-10-706-691-22
2	1045	100.0	240	16	US-10-706-691-20
3	1045	100.0	246	16	US-10-706-691-43
4	1045	100.0	298	15	US-10-432-103-4
5	1045	100.0	383	16	US-10-706-691-26
6	1045	100.0	416	16	US-10-706-691-16
7	1045	100.0	416	16	US-10-706-691-41
8	1029	98.5	416	16	US-10-706-691-18
9	1014	97.0	256	15	US-10-112-944-434
10	1014	97.0	256	15	US-10-112-944-880
11	548	52.4	110	16	US-10-706-691-24

12	548	52.4	114	16	US-10-706-691-4	Sequence 4, Appli
13	484	46.3	94	16	US-10-706-691-6	Sequence 6, Appli
14	268	25.6	450	9	US-09-909-320-320	Sequence 320, App
15	268	25.6	450	9	US-09-909-088B-320	Sequence 320, App
16	268	25.6	450	9	US-09-905-291A-320	Sequence 320, App
17	268	25.6	450	9	US-09-902-853-320	Sequence 320, App
18	268	25.6	450	9	US-09-907-824-320	Sequence 320, App
19	268	25.6	450	9	US-09-907-841-320	Sequence 320, App
20	268	25.6	450	10	US-09-904-011-320	Sequence 320, App
21	268	25.6	450	10	US-09-903-640-320	Sequence 320, App
22	268	25.6	450	10	US-09-908-093-320	Sequence 320, App
23	268	25.6	450	10	US-09-906-742-320	Sequence 320, App
24	268	25.6	450	10	US-09-906-838-320	Sequence 320, App
25	268	25.6	450	10	US-09-907-613-320	Sequence 320, App
26	268	25.6	450	10	US-09-907-942-320	Sequence 320, App
27	268	25.6	450	10	US-09-904-859-320	Sequence 320, App
28	268	25.6	450	10	US-09-909-204-320	Sequence 320, App
29	268	25.6	450	10	US-09-904-820-320	Sequence 320, App
30	268	25.6	450	10	US-09-904-786-320	Sequence 320, App
31	268	25.6	450	10	US-09-906-646-320	Sequence 320, App
32	268	25.6	450	10	US-09-906-700-320	Sequence 320, App
33	268	25.6	450	10	US-09-903-786-320	Sequence 320, App
34	268	25.6	450	10	US-09-902-903-320	Sequence 320, App
35	268	25.6	450	10	US-09-903-749A-320	Sequence 320, App
36	268	25.6	450	10	US-09-904-119-320	Sequence 320, App
37	268	25.6	450	10	US-09-904-956-320	Sequence 320, App
38	268	25.6	450	10	US-09-902-736-320	Sequence 320, App
39	268	25.6	450	10	US-09-907-794-320	Sequence 320, App
40	268	25.6	450	10	US-09-903-943-320	Sequence 320, App
41	268	25.6	450	10	US-09-904-462-320	Sequence 320, App
42	268	25.6	450	10	US-09-907-925-320	Sequence 320, App
43	268	25.6	450	10	US-09-902-692-320	Sequence 320, App
44	268	25.6	450	10	US-09-903-520-320	Sequence 320, App
45	268	25.6	450	10	US-09-905-056-320	Sequence 320, App

ALIGNMENTS

RESULT 1
US-10-706-691-22
; Sequence 22, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Pegan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 22
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-22

Query Match 100.0%; Score 1045; DB 16; Length 207;
Best Local Similarity 100.0%; Pred. No. 5e-88;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VNITSPVRLIHGTGKALLSVQYSTSSDRPVVKWQKRDKPVTVVQSIGTIGTILRP 60
Db 1 VNITSPVRLIHGTGKALLSVQYSTSSDRPVVKWQKRDKPVTVVQSIGTIGTILRP 60

QY 61 DYDRIRLFENGSLLSLDLQADGTYEVEISITDDTFTGKTKINTLVDPISRPQVLVA 120
DB 61 DYDRIRLFENGSLLSLDLQADGTYEVEISITDDTFTGKTKINTLVDPISRPQVLVA 120
QY 121 STTVLESEAFNLCSHENGTKPSYTWLKGKPLNDSRMLSPDQKVLITITVLMEDDDD 180
DB 121 STTVLESEAFNLCSHENGTKPSYTWLKGKPLNDSRMLSPDQKVLITITVLMEDDDD 180
QY 181 LYSWMVENPISQGRSLPVKITVYRRSS 207
DB 181 LYSWMVENPISQGRSLPVKITVYRRSS 207

RESULT 2

US-10-706-691-20
; Sequence 20, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 20
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-20

Query Match 100.0%; Score 1045; DB 16; Length 240;
Best Local Similarity 100.0%; Pred. No. 6.1e-88;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VNITSPVRLIHGTVGKSALLSVQYSSSTSDRPVVKWQKRDKPTVVVQSIGTEVIGTLRP 60
DB 34 VNITSPVRLIHGTVGKSALLSVQYSSSTSDRPVVKWQKRDKPTVVVQSIGTEVIGTLRP 93
QY 61 DYDRIRLFENGSLLSLDLQADGTYEVEISITDDTFTGKTKINTLVDPISRPQVLVA 120
DB 94 DYDRIRLFENGSLLSLDLQADGTYEVEISITDDTFTGKTKINTLVDPISRPQVLVA 153
QY 121 STTVLESEAFNLCSHENGTKPSYTWLKGKPLNDSRMLSPDQKVLITITVLMEDDDD 180
DB 154 STTVLESEAFNLCSHENGTKPSYTWLKGKPLNDSRMLSPDQKVLITITVLMEDDDD 213
QY 181 LYSWMVENPISQGRSLPVKITVYRRSS 207
DB 214 LYSWMVENPISQGRSLPVKITVYRRSS 240

RESULT 3

US-10-706-691-43
; Sequence 43, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula

; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 43
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-43

Query Match 100.0%; Score 1045; DB 16; Length 246;
Best Local Similarity 100.0%; Pred. No. 6.3e-88;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VNITSPVRLIHGTVGKSALLSVQYSSSTSDRPVVKWQKRDKPTVVVQSIGTEVIGTLRP 60
DB 34 VNITSPVRLIHGTVGKSALLSVQYSSSTSDRPVVKWQKRDKPTVVVQSIGTEVIGTLRP 93
QY 61 DYDRIRLFENGSLLSLDLQADGTYEVEISITDDTFTGKTKINTLVDPISRPQVLVA 120
DB 94 DYDRIRLFENGSLLSLDLQADGTYEVEISITDDTFTGKTKINTLVDPISRPQVLVA 153
QY 121 STTVLESEAFNLCSHENGTKPSYTWLKGKPLNDSRMLSPDQKVLITITVLMEDDDD 180
DB 154 STTVLESEAFNLCSHENGTKPSYTWLKGKPLNDSRMLSPDQKVLITITVLMEDDDD 213
QY 181 LYSWMVENPISQGRSLPVKITVYRRSS 207
DB 214 LYSWMVENPISQGRSLPVKITVYRRSS 240

RESULT 4

US-10-432-103-4
; Sequence 4, Application US/10432103
; Publication No. US20040043424A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dzung Aina M.
; APPLICANT: YUE, Henry
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: LU, Yan
; APPLICANT: LO, Terrence P.
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: GANDHI, Ameera R.
; APPLICANT: ARVIZU, Chandra
; APPLICANT: YAO, Monique G.
; TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS
; FILE REFERENCE: PP-0841 PCT
; CURRENT APPLICATION NUMBER: US/10/432,103
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: 60/249,645
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040043424A1 5831801CD1
US-10-432-103-4
Query Match 100.0%; Score 1045; DB 15; Length 298;

Best Local Similarity 100.0%; Pred. No. 8.1e-88;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNITSPVRLIHGTGKSAALLSVQYSSSTSDRPVVKWQIKRDKPVTVVQSIGTEVIGTLRP 60
Db 34 VNITSPVRLIHGTGKSAALLSVQYSSSTSDRPVVKWQIKRDKPVTVVQSIGTEVIGTLRP 93
Qy 61 DYDRIRLFFENGSLLLSDQLADEGTYEVEISITDDFTGKTNLTVDVPISRPQVLVA 120
Db 94 DYDRIRLFFENGSLLLSDQLADEGTYEVEISITDDFTGKTNLTVDVPISRPQVLVA 153
Qy 121 STTVLESEAFNLCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDDD 180
Db 154 STTVLESEAFNLCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDDD 213
Qy 181 LYSQWVENPISQGRSLPVKITVYRRSS 207
Db 214 LYSQWVENPISQGRSLPVKITVYRRSS 240

RESULT 5

US-10-706-691-26
; Sequence 26, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10/706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 26
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-26

Query Match 100.0%; Score 1045; DB 16; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.1e-87;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNITSPVRLIHGTGKSAALLSVQYSSSTSDRPVVKWQIKRDKPVTVVQSIGTEVIGTLRP 60
Db 1 VNITSPVRLIHGTGKSAALLSVQYSSSTSDRPVVKWQIKRDKPVTVVQSIGTEVIGTLRP 60
Qy 61 DYDRIRLFFENGSLLLSDQLADEGTYEVEISITDDFTGKTNLTVDVPISRPQVLVA 120
Db 61 DYDRIRLFFENGSLLLSDQLADEGTYEVEISITDDFTGKTNLTVDVPISRPQVLVA 120
Qy 121 STTVLESEAFNLCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDDD 180
Db 121 STTVLESEAFNLCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDDD 180
Qy 181 LYSQWVENPISQGRSLPVKITVYRRSS 207
Db 181 LYSQWVENPISQGRSLPVKITVYRRSS 207

RESULT 6

US-10-706-691-16
; Sequence 16, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:

; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10/706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 16
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-16

Query Match 100.0%; Score 1045; DB 16; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.3e-87;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNITSPVRLIHGTGKSAALLSVQYSSSTSDRPVVKWQIKRDKPVTVVQSIGTEVIGTLRP 60
Db 34 VNITSPVRLIHGTGKSAALLSVQYSSSTSDRPVVKWQIKRDKPVTVVQSIGTEVIGTLRP 93
Qy 61 DYDRIRLFFENGSLLLSDQLADEGTYEVEISITDDFTGKTNLTVDVPISRPQVLVA 120
Db 94 DYDRIRLFFENGSLLLSDQLADEGTYEVEISITDDFTGKTNLTVDVPISRPQVLVA 153
Qy 121 STTVLESEAFNLCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDDD 180
Db 154 STTVLESEAFNLCSHENGTKPSYTWLKDGPPLNDSRMLLSPDQKVLITITRVLMEDDD 213
Qy 181 LYSQWVENPISQGRSLPVKITVYRRSS 207
Db 214 LYSQWVENPISQGRSLPVKITVYRRSS 240

RESULT 7

US-10-706-691-41
; Sequence 41, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Fagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Power, Christine
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10/706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 41
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-41

Query Match 100.0%; Score 1045; DB 16; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.3e-87;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APPLICANT: Ghosh, Malabika
APPLICANT: Wang, Dunrui
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Zhiwei
TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
Secreted Polypeptides
FILE REFERENCE: 805A
CURRENT APPLICATION NUMBER: US/10/112,944
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: US 09/519,705
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 09/552,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 09/577,408
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 924
SOFTWARE: pt_FL_genes Version 5.0
SEQ ID NO 880
LENGTH: 256
TYPE: PRT
ORGANISM: Homo sapiens
US-10-112-944-880

Query Match 97.0%; Score 1014; DB 15; Length 256;
Best Local Similarity 96.6%; Pred. No. 4.7e-85;
Matches 200; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Qy 1 VNITSPVRLIHGTGKSAALLSVQYSSSTSSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 60
Db 34 VNITSPVRLIHGTGKSAALLSVQYSSSTSSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 93
Qy 61 DYDRIRLRFENGSLLSLDQLADEGTYEVEISITDDTFTGKTNLTVDVPIRQVLVA 120
Db 94 DYDRIRLRFENGSLLSLDQLADEGTYEVEISITDDTFTGKTNLTVDVPIRQVLGA 153
Qy 121 STTVLEISEATLNCSEHGKPSYTWLKGKPLNDSRMLSPDQKVLITRVLMEDDD 180
Db 154 STTVLEISEATLNCSEHGKPSYTWLKGKPLNDSRMLSPDQKVLITRVLMEDDD 213
Qy 181 LYSWVENPIQGRSLPVKITVYRRSS 207
Db 214 LYSWVENPINQGRSLPVKITVYRKSS 240

RESULT 11
US-10-706-691-24
Sequence 24, Application US/10706691
Publication No. US20040204352A1
GENERAL INFORMATION:
APPLICANT: Davids, Andrew Robert
APPLICANT: Fagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Power, Christine
APPLICANT: Chvatchko, Yolande
APPLICANT: Boschert, Ursula
TITLE OF INVENTION: Cytokine antagonist molecules
FILE REFERENCE: 674582-2001
CURRENT APPLICATION NUMBER: US/10/706,691
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/GB03/01851
PRIOR FILING DATE: 2003-04-30
PRIOR APPLICATION NUMBER: GB 0209884.6
PRIOR FILING DATE: 2002-04-30

NUMBER OF SEQ ID NOS: 43
SOFTWARE: SeqWin99, version 1.02
SEQ ID NO 24
LENGTH: 110
TYPE: PRT
ORGANISM: Homo sapiens
US-10-706-691-24

Query Match 52.4%; Score 548; DB 16; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VNITSPVRLIHGTGKSAALLSVQYSSSTSSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 60
Db 1 VNITSPVRLIHGTGKSAALLSVQYSSSTSSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 60
Qy 61 DYDRIRLRFENGSLLSLDQLADEGTYEVEISITDDTFTGKTNLTVDV 110
Db 61 DYDRIRLRFENGSLLSLDQLADEGTYEVEISITDDTFTGKTNLTVDV 110

RESULT 12
US-10-706-691-4
Sequence 4, Application US/10706691
Publication No. US20040204352A1
GENERAL INFORMATION:
APPLICANT: Davids, Andrew Robert
APPLICANT: Fagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Power, Christine
APPLICANT: Chvatchko, Yolande
APPLICANT: Boschert, Ursula
TITLE OF INVENTION: Cytokine antagonist molecules
FILE REFERENCE: 674582-2001
CURRENT APPLICATION NUMBER: US/10/706,691
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/GB03/01851
PRIOR FILING DATE: 2003-04-30
PRIOR APPLICATION NUMBER: GB 0209884.6
PRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 43
SOFTWARE: SeqWin99, version 1.02
SEQ ID NO 4
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-10-706-691-4

Query Match 52.4%; Score 548; DB 16; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.4e-42;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VNITSPVRLIHGTGKSAALLSVQYSSSTSSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 60
Db 5 VNITSPVRLIHGTGKSAALLSVQYSSSTSSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 64
Qy 61 DYDRIRLRFENGSLLSLDQLADEGTYEVEISITDDTFTGKTNLTVDV 110
Db 65 DYDRIRLRFENGSLLSLDQLADEGTYEVEISITDDTFTGKTNLTVDV 114

RESULT 13
US-10-706-691-6
Sequence 6, Application US/10706691
Publication No. US20040204352A1
GENERAL INFORMATION:
APPLICANT: Davids, Andrew Robert
APPLICANT: Fagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Power, Christine
APPLICANT: Chvatchko, Yolande
APPLICANT: Boschert, Ursula
TITLE OF INVENTION: Cytokine antagonist molecules

```

; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10/706.691
; PRIOR FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 6
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-6

Query Match      46.3%; Score 484; DB 16; Length 94;
Best Local Similarity 100.0%; Pred. No. 8.3e-37;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 PISRPQVLVASTTVEISEAFTLNCSEHGKPSYTWLKGKPLNDSRMLLSPDQKVL 170
Db 1 PISRPQVLVASTTVEISEAFTLNCSEHGKPSYTWLKGKPLNDSRMLLSPDQKVL 60

Qy 171 ITRVLMEDDDLYSCWENPISQGRSLPVKITVYR 204
Db 61 ITRVLMEDDDLYSCWENPISQGRSLPVKITVYR 94

RESULT 14
US-09-909-320-320
; Sequence 320, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08

; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10/706.691
; PRIOR FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 320
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-909-320-320

Query Match      25.6%; Score 268; DB 9; Length 450;
Best Local Similarity 31.9%; Pred. No. 5.1e-16;
Matches 67; Conservative 43; Mismatches 90; Indels 10; Gaps 7;

Qy 1 VNITSPVRLIHGTGKSALESVOYS--STSSDRPVVKWQLKR--DKPVTVVQSIGTEVIG 56
Db 20 LKVTVPSTHTVHGVRGQALYLVHVGFTHTPASDIQII-WLPERPHTMPKYLKSGVNSVVP 78

Qy 57 TLRPDYDRIRLP-ENGSLLLSDLOADEGTYEVSIT-DDFTTGEKTNLTVDVPISR 114
Db 79 DL--EYQHKFTMPPNPNASLLINLPDPDEGNYIVKVNIOGNGTSLASQKIQTVDVDTK 136

Qy 115 POVLV-ASTTVLELSEAFNLCSHGKPSYTWLKGKPLNDSRMLLSPDQKVLITR 173
Db 137 PVQIHPPSGAVEYVGNWTLTCHVEGTRLAYQWLKNGRPVHTTSSTYSFSPQNTLHIAP 196

Qy 174 VLMEDDDLSCWENPISQGRSLPVKITVY 203
Db 197 VTKEDIGNYSCLVRNPVSEMSDIIMPIY 226

RESULT 15
US-09-909-088B-320
; Sequence 320, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 15:58:02; Search time 11.9615 Seconds
(without alignments)
1665.085 Million cell updates/sec

Title: US-10-706-691-22
Perfect score: 1045
Sequence: 1 VNITSPVRLIHGTGKSALL.....NPISQGRSLPVKITVYRRSS 207
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	207.5	19.9	278	2 JC1506	biliary glycoprote
2	207.5	19.9	341	2 JC1512	biliary glycoprote
3	202.5	19.4	278	2 A39037	carcinoembryonic a
4	186	17.8	458	2 JC1509	biliary glycoprote
5	181	17.3	521	2 S34338	biliary glycoprote
6	180.5	17.3	629	2 A46500	Ly-9.2 antigen - m
7	179.5	17.2	272	2 I48268	biliary glycoprote
8	179.5	17.2	278	2 JC1507	biliary glycoprote
9	179.5	17.2	341	2 JC1511	biliary glycoprote
10	176.5	16.9	475	2 A54879	pregnancy-specific
11	167	16.0	853	1 IJBONC	neural cell adhesi
12	166	15.9	858	1 IJTNCC	neural cell adhesi
13	165	15.8	475	2 I76668	pregnancy-specific
14	164	15.7	458	2 S68177	C-CAM2a protein is
15	164	15.7	458	2 S23969	cell-adhesion mole
16	164	15.7	519	2 A44783	ecto-ATPase precu
17	161	15.4	458	1 WMMSR1	biliary glycoprote
18	161	15.4	521	2 JC1508	biliary glycoprote
19	160.5	15.4	725	2 JE0100	neural cell adhesi
20	160.5	15.4	1092	1 JN0635	neural cell adhesi
21	159	15.2	344	2 A27681	non-specific cross-
22	158.5	15.2	709	2 A35364	carcinoembryonic a
23	157	15.0	299	2 S56749	junctional adhesio
24	156.5	15.0	761	1 IJHUNG	neural cell adhesi
25	155	14.8	324	2 G43354	pregnancy-specific
26	155	14.8	326	2 F43354	pregnancy-specific
27	155	14.8	332	2 A43354	pregnancy-specific
28	155	14.8	335	2 H43354	pregnancy-specific
29	155	14.8	395	2 D43354	pregnancy-specific

30	155	14.8	397	2 C43354	pregnancy-specific
31	155	14.8	406	2 E43354	pregnancy-specific
32	155	14.8	417	2 A28277	pregnancy-specific
33	155	14.8	419	2 A33258	pregnancy-specific
34	155	14.8	419	2 A31135	pregnancy-specific
35	155	14.8	426	2 A35964	pregnancy-specific
36	155	14.8	426	2 A33258	pregnancy-specific
37	155	14.8	426	2 A35341	pregnancy-specific
38	155	14.8	428	2 A27658	pregnancy-specific
39	154.5	14.8	725	2 JE0099	neural cell adhesi
40	154.5	14.8	1091	1 IJCHNL	neural cell adhesi
41	154	14.7	206	2 A40305	biliary glycoprote
42	154	14.7	321	2 JH0395	biliary glycoprote
43	154	14.7	351	2 JH0396	biliary glycoprote
44	154	14.7	417	2 JH0394	biliary glycoprote
45	154	14.7	419	2 B54312	pregnancy-specific

ALIGNMENTS

RESULT 1

JC1506
biliary glycoprotein B - mouse
C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C:Accession: JC1506
R:McCuig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
A:Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopro
A:Reference number: JC1505; MUID:93273228; PMID:8500759
A:Accession: JC1506
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-278 <MCC>
A:Cross-references: UNIPROT:Q99232
C:Comment: This protein is expressed at the cell surface and plays a determinant role in
C:Genetics:
A:Gene: BGPB
C:Superfamily: biliary glycoprotein; carcinoembryonic antigen precursor amino-terminal h
C:Keywords: glycoprotein; receptor
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CRAN>
F:159-216/Domain: immunoglobulin homology <IMM>
F:87,104,153,195/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	19.9%	Score	207.5;	DB	2;	Length	278;
Best Local Similarity	32.1%;	Pred. No.	3.5e-09;				
Matches	54;	Conservative	32;	Mismatches	73;	Indels	9;
		Gaps	5;				
Qy	40	RDXPTVVQSIGTEVIGTLR----	PDYRDRIRLPFENGSLLLSDIQLADEGTYEVEISITD	95			
Db	69	KGNPVSNAEIVHQVTGNTKTTTGPASGRETIVYNSGSLIIQRTVTKDTGVYTTIE--MTD	126				
Qy	96	DTP-TGSEKTLINLTVDVPIRSPQVLVASTTVLELSEAFITLNCSHENGTPKPSYTWLKDQKPL	154				
Db	127	ENFRTEATVQHVHQVPTQPSLQVTTNTVKEL-DSVTLTCL-SNDIGANIQLWLFNSQSL	184				
Qy	155	LNDSRMLLSPDQKVLITTRVLMEDDDLYSCWENPISQGRSLPVKITV	202				
Db	185	QLTERMTLQNSNLTIRIDPIKREDAGEYQCEISNPNVSVKRSNSIKLDI	232				

RESULT 2

JC1512
biliary glycoprotein H - mouse
C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C:Accession: JC1512
R:McCuig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
A:Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopro
A:Reference number: JC1505; MUID:93273228; PMID:8500759
A:Accession: JC1512


```

QY 181 LSCWVENPISQGRSLPVKITV 202
Db 211 EYQCEISNPVSVRSNSIKLDI 232

RESULT 9
JC1511
biliary glycoprotein G - mouse
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: JC1511
R;McCuaign, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
A;Title: Expression of the Bgp gene and characterization of mouse colon biliary glycoprotein G
A;Reference number: JC1505; MUID:93273228; PMID:8500759
A;Accession: JC1511
A;Molecule type: DNA
A;Residues: 1-341 <MCC>
A;Cross-references: UNIPROT:Q61353; GB:X67282
C;Comment: This protein is expressed at the cell surface and plays a determinant role in
C;Genetics:
A;Gene: Bgpg
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal
C;Keywords: glycoprotein; receptor
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;75-124/Domain: immunoglobulin homology <IMM1>
F;159-216/Domain: immunoglobulin homology <IMM2>
F;71,89,104,153,195/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.2%; Score 179.5; DB 2; Length 341;
Best Local Similarity 31.7%; Pred. No. 7.6e-07;
Matches 45; Conservative 29; Mismatches 63; Indels 5; Gaps 4;

QY 62 YRDRIRLFENGSLLDLQADEGYEVEISITDPTF-TGEKTLNLTVDVPIRSPQVLVA 120
Db 95 YSGREIIYVSGSLLFQMTKMDGVYTLT--MTDENRYRQTQATVRFHVHPVTPFPFLQVT 152

QY 121 STTVLELSEAFNLCSHENGTKPSYTWLKGKPLNDSRMLSPDQKVLITITRVLMEDDDD 180
Db 153 NTTVKEL-DSVTLTCL--SNDIGANIQLFNSQSLQLTERMTLSQNNILRIDPIKREDAG 210

QY 181 LSCWVENPISQGRSLPVKITV 202
Db 211 EYQCEISNPVSVRSNSIKLDI 232

RESULT 10
A54879
pregnancy-specific glycoprotein rncgm3 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C;Accession: A54879
R;Chen, H.; Chen, C.L.; Chou, J.Y.
Biochemistry 33, 9615-9626, 1994
A;Title: Characterization of two promoters of a rat pregnancy-specific glycoprotein gene
A;Reference number: A54879; MUID:94347731; PMID:8068638
A;Accession: A54879
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-475 <CHE>
A;Cross-references: UNIPROT:Q62664; GB:U09815; NID:q497254; PIDN:AAA56870.1; PID:g497255
A;Note: authors translated the codon GCT for residue 64 as Gly
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal
C;Keywords: glycoprotein
F;1-137/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA1>
F;242-378/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA2>
F;399-456/Domain: immunoglobulin homology <IMM2>

Query Match 16.9%; Score 176.5; DB 2; Length 475;
Best Local Similarity 32.3%; Pred. No. 2e-06;
Matches 64; Conservative 24; Mismatches 95; Indels 15; Gaps 8;

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QY 11 HGTGKSAALLSVQYSSTSSDRPVVKW-----QLKRDKPVTVVQSIGTEVIGTLRDPYDR 65
Db 284 HAVEGESVLLYH--NLPEALQTFSWYKGVYSLKEFK--IAEYSIATKSVPF-GPAHRGR 338

QY 66 IRLFENGSLLDLQADEGYEVEISITDPTFTGKTLNLTVDVPIRSPQVLVA--TTV- 124
Db 339 ATGYTNGSLLDLQDLTARDTGLYTL-VTLDSNSIKSAPVQVTVHKPQVFLFRTVESTVT 397

QY 125 LELSEAFNLCSHENGTKPSYTWLKGKPLNDSRMLSPDQKVLITITRVLMEDDDDLYSC 184
Db 398 VOSSVVFV--CLSDN-TGVSIRLWFKNQNLQVTERMTLSQNNILRIDVRRREDAGQYRC 454

QY 185 MVENPISQGRSLPVKITV 202
Db 455 EAFNPISSTSRPVSLAV 472

RESULT 11
IJBONC
neural cell adhesion molecule short domain form precursor - bovine
N;Alternate names: NCAM-140
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession: A32976; A38778; B44290; S05402
R;Lipkin, V.M.; Khramtsov, N.V.; Andreeva, S.G.; Moshnyakov, M.V.; Petukhova, G.V.; Rakit
FEBS Lett. 254, 69-73, 1989
A;Title: Calmodulin-independent bovine brain adenylylate cyclase. Amino acid sequence and
A;Reference number: A32976; MUID:89378239; PMID:2776887
A;Accession: A32976
A;Molecule type: mRNA
A;Residues: 1-853 <LIP>
A;Cross-references: UNIPROT:P31836; GB:X16451; NID:960; PIDN:CAA34470.1; PID:g61
A;Accession: A38778
A;Molecule type: protein
A;Residues: 20-35;51-61;113-117;122-147;155-161;262-275;279-302;353-360;369-382;544-562;5
A;Note: the authors identified this protein as calmodulin-independent adenylylate cyclase
R;Rougon, G.; Marshak, D.R.
J. Biol. Chem. 261, 3396-3401, 1986
A;Title: Structural and immunological characterization of the amino-terminal domain of ma
A;Reference number: A44290; MUID:86140120; PMID:3512556
A;Accession: B44290
A;Molecule type: protein
A;Residues: 20-36 <ROU>
A;Note: 23-Glu was also found
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mole
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; sial
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-853/Product: neural cell adhesion molecule, short domain form #status experimental <
F;20-719/Domain: extracellular #status predicted <EXT>
F;34-98/Domain: immunoglobulin homology <IMM1>
F;132-191/Domain: immunoglobulin homology <IMM2>
F;152-156/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;228-288/Domain: immunoglobulin homology <IMM3>
F;261-270/Region: NCAM binding #status predicted
F;321-396/Domain: immunoglobulin homology <IMM4>
F;428-490/Domain: immunoglobulin homology <IMM5>
F;527-604/Domain: fibronectin type III repeat homology <FN3A>
F;633-693/Domain: fibronectin type III repeat homology <FN3B>
F;720-737/Domain: transmembrane #status predicted <TM>
F;738-853/Domain: intracellular #status predicted <INT>
F;41-96,139-189,235-286,328-394,435-488/Disulfide bonds: #status predicted
F;222,314,346,432,458,487/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.0%; Score 167; DB 1; Length 853;
Best Local Similarity 30.9%; Pred. No. 2.4e-05;
Matches 55; Conservative 28; Mismatches 73; Indels 22; Gaps 7;

QY 28 SSRRPVVWQLKDKPVTVVQSIGTEVIGTLRDPYDRIRLFENGSLLDLQADEGTY 87
Db 143 SSLPPTIIWKHK-----GRDVI--LKKDV--RFIVLTNNYLQIRGIKKTDEGTY 187

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QY 88 EVEISITDDTFTGKTNLTVDVP--ISRPOVLVASTTVLESLSAFTLNCSHENGTKPSY 145
DB 188 RCEGRILARGEINFKDIQVNVNPTVQARQSIYNATA--NLGQSVTLVCNAGPEPTV 245
QY 146 TWLKDQKPLLN---DSRMLLSPQKVLTTIRVLMEDDDLYSCMVNPI-SQGRSLPVKI 200
DB 246 SWTKDGEQIENEEDBKLYFSDSSBELTIRKVDKNDEAEYVCIENKAGEQDASIHVKV 303

RESULT 12

Neural cell adhesion molecule short domain form precursor - rat
N/Alternate names: NCAM-140
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
C/Accession: S00846; B37795; I58136
R/Small, S.J.; Shull, G.E.; Santoni, M.J.; Akesson, R.
J. Cell Biol. 105, 2335-2345, 1987
A/Title: Identification of a cDNA clone that contains the complete coding sequence for a
A/Reference number: S00846; MUID:88059265; PMID:3680385
A/Accession: S00846
A/Molecule type: mRNA
A/Residues: 1-858 <SMA>
A/Cross-references: UNIPROT:P13596; EMBL:X06564
R/Small, S.J.; Akesson, R.
J. Cell Biol. 111, 2089-2096, 1990
A/Title: Expression of the unique NCAM VASE exon is independently regulated in distinct
A/Reference number: A37795; MUID:91035620; PMID:1699951
A/Accession: B37795
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 340-381 <SM2>
R/Small, S.J.; Haines, S.L.; Akesson, R.A.
Neuron 1, 1007-1017, 1988
A/Title: Polypeptide variation in an N-CAM extracellular immunoglobulin-like fold is dev
A/Reference number: I58136; MUID:90166485; PMID:2483093
A/Accession: I58136
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 353-364 <RES>
A/Cross-references: GB:M32611; NID:g205643; PIDN:AAA41679.1; PID:g205644
C/Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C/Comment: Various forms of NCAM are produced by alternative splicing.
C/Genetics:
A/Gene: NCAM
C/Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C/Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-858/Product: neural cell adhesion molecule, short domain form #status predicted <MA
F/20-721/Domain: extracellular #status predicted <EXT>
F/34-98/Domain: immunoglobulin homology <IMM1>
F/132-191/Domain: immunoglobulin homology <IMM2>
F/152-156/Region: heparin binding #status predicted
F/161-165/Region: heparin binding #status predicted
F/228-290/Domain: immunoglobulin homology <IMM3>
F/263-272/Region: NCAM binding #status predicted
F/323-398/Domain: immunoglobulin homology <IMM4>
F/430-492/Domain: immunoglobulin homology <IMM5>
F/529-606/Domain: fibronectin type III repeat homology <FN3A>
F/635-695/Domain: fibronectin type III repeat homology <FN3B>
F/722-739/Domain: intracellular #status predicted <TM>
F/740-858/Domain: transmembrane #status predicted <INT>
F/41-96,139-189,235-288,330-396,437-490/Disulfide bonds: #status predicted
F/222,316,348,434,460,489/Banding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.9%; Score 166; DB 1; Length 858;
Best Local Similarity 30.0%; Pred. No. 2.9e-05;
Matches 54; Conservative 28; Mismatches 74; Indels 24; Gaps 7;

QY 28 SSDRPVVKWQKRDKPVTWVQSIGTEVIGTIRPYDRIRLRFENGSLLSLDLADEGTY 87
DB 143 SSLPPTIWKHK-----GRDVI--LKKDV--RFVLSNNYLQIRIGIKKTDEGTY 187

QY 88 EVEISITDDTFTGKTNLTVDVP--ISRPOVLVASTTVLESLSAFTLNCSHENGTKPSY 145
DB 188 RCEGRILARGEINFKDIQVNVNPTVQARQSIYNATA--NLGQSVTLVCADGPEPTM 245
QY 146 TWLKDQKPLLN---DSRMLLSPQKVLTTIRVLMEDDDLYSCMVNPI-SQGRSLPVKI 200
DB 246 SWTKDGEPIENEEDDEKHIFSDSSBELTIRNVKNDDEAEYVCIENKAGEQDASIHVKV 305

RESULT 13

176668
pregnancy-specific glycoprotein - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Aug-1996 #sequence revision 02-Aug-1996 #text_change 09-Jul-2004
C/Accession: I76668
R/Rudert, F.; Saunders, A.M.; Thompson, J.A.; Rebstock, S.; Zimmermann, W.A.
Mamm. Genome 3, 262-273, 1992
A/Title: Characterization of murine carcinoembryonic antigen gene family members.
A/Reference number: I57007; MUID:92345715; PMID:1638085
A/Accession: I76668
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-475 <RES>
A/Cross-references: UNIPROT:Q62056; GB:M83344; NID:g200316; PIDN:AAA39916.1; PID:g200317
C/Genetics:
A/Gene: CGM5
C/Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C/Keywords: glycoprotein
F/1-137/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA1>
F/399-456/Domain: immunoglobulin homology <IMM>

Query Match 15.8%; Score 165; DB 2; Length 475;

Best Local Similarity 33.1%; Pred. No. 1.6e-05;
Matches 52; Conservative 26; Mismatches 69; Indels 10; Gaps 5;

QY 49 SIGTE--VIGTLRPDYDRIRLRFENGSLLSLDLADEGTYEVRISITDDTFTGKTNL 106
DB 323 SIATKSIIMGVAR---SRRETIVYNGSLLDQVTEKDSGVVTL---ITDSNMGVEIAHV 376
QY 107 TVDV-PTSRPOVLVASTTVLESLSAFTLNCSHENGTKPSYTWLKDQKPLNDSRMLSPD 165
DB 377 QVNVKHLATQPKATDSTVRVQGSVFTFCPSDN-TGVSIRWLFNNORLQTLTERMTLSPS 435

QY 166 QKVLTTIRVLMEDDDLYSCMVNPI-SQGRSLPVKITY 202

DB 436 KCOLWIFTRKEDAGEYOCEAFNPVSKTSLPVLAV 472

RESULT 14

S68177
C-CAM2a protein isoform precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 15-Feb-1997 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S68177
R/Lucka, L.; Cichocka, I.; Baeumler, K.; Bechler, K.; Reutter, W.
Eur. J. Biochem. 234, 527-535, 1995
A/Title: A short isoform of carcinoembryonic-antigen-related rat liver cell-cell adhesio
A/Reference number: S68177; MUID:96128184; PMID:8536699
A/Accession: S68177
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-458 <IUC>
A/Cross-references: UNIPROT:Q63093; EMBL:X91137; NID:g1160272; PIDN:CAA62577.1; PID:g1161
C/Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
F/1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA>
F/1-33/Domain: signal sequence #status predicted <SIG>
F/34-458/Product: C-CAM2a protein isoform #status predicted <MAT>
F/252-301/Domain: immunoglobulin homology <IMM>

Query Match 15.7%; Score 164; DB 2; Length 458;
Best Local Similarity 32.6%; Pred. No. 1.9e-05;
Matches 42; Conservative 24; Mismatches 61; Indels 2; Gaps 2;

QY 74 LLLSDLQADRGTYEVEISITDDTFTGCKTINLTVDVPISRPOVLVASTTVLSEAFTL 133
 Db 284 LFIISNITNNSGTYACFVNNTVGLSRRTVKNTVFEPVTPQSIQINTTVKELG-SVTL 342

QY 134 NCSENGTKPSYTWLKGKPLNDSRMLLPDQKVLTRITRVLMEDDDLYSCWVENPISQ 193
 Db 343 TCFSKD-TGVSVRWLFNSQSLQTLDRMTLSQDNSTLRIDPIKREDAGDYQCEISNPVSFR 401

QY 194 RSLPVKITV 202
 Db 402 ISHPIKLDV 410

Search completed: July 26, 2005, 16:14:16
 Job time : 12.9615 secs

QY 194 RSLPVKITV 202
 Db 402 ISHPIKLDV 410

RESULT 15

S23969
 cell-adhesion molecule short form (cell-CAM105) - rat
 N/Alternate names: C-CAM protein
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 22-Nov-1993 #sequence revision 01-Sep-1995 #text_change 09-Jul-2004
 C/Accession: S23969; S32483; S38826; S10563; S32102
 R/Culic, O.; Huang, Q.H.; Flanagan, D.; Hixson, D.; Lin, S.H.
 Biochem. J. 285, 47-53, 1992
 A/Title: Molecular cloning and expression of a new rat liver cell-CAM105 isoform. Differ
 A/Reference number: S23969; MUID:92344597; PMID:1637321
 A/Accession: S23969
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-458 <CUL>
 A/Cross-references: UNIPROT:P16573; EMBL:Z12019; NID:955858; PIDN:CAA78054.1; PID:g55859
 R/Edlund, M.; Gaardsvoll, H.; Bock, E.; Oebrick, B.
 Eur. J. Biochem. 213, 1109-1116, 1993
 A/Title: Different isoforms and stock-specific variants of the cell adhesion molecule C-
 A/Reference number: S32483; MUID:93279310; PMID:8504806
 A/Accession: S32483
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-458 <EDL>
 A/Cross-references: EMBL:X71122; NID:g287819; PIDN:CAA50435.1; PID:g287820
 R/Cheung, P.H.; Culic, O.; Qiu, Y.; Earley, K.; Thompson, N.; Hixson, D.C.; Lin, S.H.
 Biochem. J. 295, 427-435, 1993
 A/Title: The cytoplasmic domain of C-CAM is required for C-CAM-mediated adhesion functio
 A/Reference number: S38826; MUID:94058980; PMID:8240240
 A/Accession: S38826
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-48, 'K', '50-54', 'A', '56-69', 'G', '71-72', 'LNPD', '77-85', 'D', '87', 'M', '89', 'K', '91', 'G', '93-
 A/Cross-references: EMBL:M92848; NID:g203366; PIDN:AAA16783.1; PID:g203367
 R/Aurivillius, M.; Hansen, O.C.; Lazrek, M.B.S.; Bock, E.; Oebrick, B.
 FEBS Lett. 264, 267-269, 1990
 A/Title: The cell adhesion molecule cell-CAM 105 is an ecto-ATPase and a member of the i
 A/Reference number: S10563; MUID:90292222; PMID:2141577
 A/Accession: S10563
 A/Molecule type: protein
 A/Residues: 'X', '58-66', 'A', '68,121-124', 'F', '126', 'Q', '128-134', 'X', '136-138', 'X', '356-360', 'X', '362
 A/Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
 F/1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
 F/160-217/Domain: immunoglobulin homology <IMM1>
 F/252-301/Domain: immunoglobulin homology <IMM2>
 F/337-394/Domain: immunoglobulin homology <IMM3>

Query Match 15.7%; Score 164; DB 2; Length 458;
 Best Local Similarity 32.6%; Pred. No. 1.9e-05;
 Matches 42; Conservative 24; Mismatches 61; Indels 2; Gaps 2;

QY 74 LLLSDLQADRGTYEVEISITDDTFTGCKTINLTVDVPISRPOVLVASTTVLSEAFTL 133
 Db 284 LFIISNITNNSGTYACFVNNTVGLSRRTVKNTVFEPVTPQSIQINTTVKELG-SVTL 342

QY 134 NCSENGTKPSYTWLKGKPLNDSRMLLPDQKVLTRITRVLMEDDDLYSCWVENPISQ 193
 Db 343 TCFSKD-TGVSVRWLFNSQSLQTLDRMTLSQDNSTLRIDPIKREDAGDYQCEISNPVSFR 401

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 15:57:23 ; Search time 52.996 Seconds
(without alignments)
2000.159 Million cell updates/sec

Title: US-10-706-691-22
Perfect score: 1045
Sequence: 1 VNITSPVRLIHGTGKALL.....NPISQGRSLPVKITVYRRSS 207

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1045	100.0	416	2	Q67IP8
2	1041	99.6	416	2	Q8N713
3	1032	98.8	367	2	Q6ZWL4
4	1029	98.5	413	2	Q640R3
5	268	25.6	450	2	Q6UX10
6	202.5	19.4	341	2	Q61354
7	202.5	19.4	341	2	Q6UY47
8	189.5	18.1	292	2	Q75296
9	185.5	17.8	235	2	Q61351
10	181	17.3	458	2	Q61351
11	181	17.3	521	2	Q61352
12	180.5	17.3	538	2	Q8C9B4
13	180.5	17.3	645	2	Q6N2B6
14	180.5	17.3	649	2	Q7TMP7
15	180.5	17.3	654	1	LX9_MOUSE
16	179.5	17.2	272	2	Q8R1N5
17	179.5	17.2	340	2	Q61349
18	177.5	17.0	278	2	Q61350
19	177.5	17.0	341	2	Q61353
20	176.5	16.9	475	2	Q62664
21	173.5	16.6	475	2	Q810J1
22	172.5	16.5	475	2	P70161
23	171.5	16.4	471	2	Q9DAY5
24	170.5	16.3	234	2	Q78T27
25	169	16.2	325	2	Q95791
26	168.5	16.1	365	2	Q6VAN5
27	168.5	16.1	372	2	Q6VAN6
28	168.5	16.1	429	2	Q6VAN7
29	168.5	16.1	436	2	Q6VAN8
30	168	16.1	284	2	Q9NX42
31	168	16.1	327	2	Q96IQ7

32	168	16.1	448	2	Q9JHL7	Q9jhl7 rattus norv
33	167.5	16.0	300	2	Q9JHV1	Q9jhy1 rattus norv
34	167	16.0	520	2	Q925P2	Q925p2 mus musculu
35	167	16.0	853	1	NCAL_BOVIN	P31836 bos taurus
36	166.5	15.9	471	2	Q9D2U0	Q9d2u0 mus musculu
37	166.5	15.9	476	2	Q9R038	Q9r038 mus musculu
38	166	15.9	838	2	Q8BQ96	Q8bq96 mus musculu
39	166	15.9	838	2	Q8C4B2	Q8c4b2 mus musculu
40	166	15.9	858	1	NCAL_RAT	P13596 rattus norv
41	165.5	15.8	229	2	Q9R121	Q9r121 rattus norv
42	165	15.8	475	2	Q62056	Q62056 mus musculu
43	164.5	15.7	368	2	Q6RWT3	Q6rwt3 bos taurus
44	164.5	15.7	375	2	Q6RWT4	Q6rwt4 bos taurus
45	164.5	15.7	386	2	Q60962	Q60962 mus musculu

ALIGNMENTS

RESULT 1
Q67IP8
ID Q67IP8 PRELIMINARY; PRT; 416 AA.
AC Q67IP8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Shen S., Moh M.C.;
RT "A gene related to human hepatocellular carcinoma.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY047587; AAQ93018.1; -
DR InterPro; IPR003599; Ig_2.
DR InterPro; IPR007110; Ig_LIKE.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IGC2; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Hypothetical protein.
SQ SEQUENCE 416 AA; 46055 MW; 7B8882298BBB4ABF CRC64;

Query Match 100.0%; Score 1045; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 3.9e-74;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	VNITSPVRLIHGTGKALLSVQYSTSSDRPVVKQWKDKPKVTVVQSIGTEVIGTLRP 60
Db	34	VNITSPVRLIHGTGKALLSVQYSTSSDRPVVKQWKDKPKVTVVQSIGTEVIGTLRP 93
Qy	61	DYDRIRLRFNGSLLSLDLADEGTYEVEISITDDTFTGCKTINLTVDVPISRPQLVA 120
Db	94	DYDRIRLRFNGSLLSLDLADEGTYEVEISITDDTFTGCKTINLTVDVPISRPQLVA 153
Qy	121	STTVLSEAFTLNCSHENGTKPSYTWLKDGPILLNDSRMLLSPDQKVLITRVLMDDD 180
Db	154	STTVLSEAFTLNCSHENGTKPSYTWLKDGPILLNDSRMLLSPDQKVLITRVLMDDD 213
Qy	181	LYSCWVENPISQGRSLPVKITVYRRSS 207
Db	214	LYSCWVENPISQGRSLPVKITVYRRSS 240

RESULT 2
Q8N713
ID Q8N713 PRELIMINARY; PRT; 416 AA.
AC Q8N713;

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DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein FLJ25530.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC
RP TISSUE=Brain;
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
RA Nagai K., Isogai T., Sugano S.;
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK098396; BAC05297.1; -.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00408; Igc2; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
SQ SEQUENCE 416 AA; 45994 MW; 47120CA9A00BE1CF CRC64;
Query Match 99.6%; Score 1041; DB 2; Length 416;
Best Local Similarity 99.5%; Pred. No. 8e-74; Mismatches 0; Indels 0; Gaps 0;
Matches 206; Conservative 1;
QY 1 VNITSPVRLIHGTGKSGALLSVQSSSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 60
DB 34 VNITSPVRLIHGTGKSGALLSVQSSSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 93
QY 61 DYDRIRLFENGSLLSLDLQADSGTYEVEISITDDTFTGKKTINLTVDVPISRPQVLVA 120
DB 94 DYDRIRLFENGSLLSLDLQADSGTYEVEISITDDTFTGKKTINLTVDVPISRPQVLVA 153
QY 121 STTVLESEAFTLNCSHENGTPKSYTWLKGKPLNDSRMLLSPDQKVLITITRVLMEDDD 180
DB 154 STTVLESEAFTLNCSHENGTPKSYTWLKGKPLNDSRMLLSPDQKVLITITRVLMEDDD 213
QY 181 LYSCWVENPISQGRSLPVKITVYRRSS 207
DB 214 LYSCWVENPISQGRSLPVKITVYRRSS 240
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Q6ZWL4 PRELIMINARY; PRT; 367 AA.
ID Q6ZWL4
AC Q6ZWL4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ16002.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC TISSUE=Brain;
RA Suzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Shiohata N.,
RA Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,
RA Matsumura Y., Moriya S., Chiba E., Momiyama H., Onogawa S.,
RA Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Katsoka R.,
RA Kuga N., Kuroda A., Satoh I., Kanata K., Takami S., Terashima Y.,
RA Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T.,
RA Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K.,
RA Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y.,
RA Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RA Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RL

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DR EMBL; AK125595; BAC85486.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG-.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00408; Igc2; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Receptor.
SQ SEQUENCE 367 AA; 40456 MW; 35956FA245A408F0 CRC64;
Query Match 98.8%; Score 1032; DB 2; Length 367;
Best Local Similarity 99.0%; Pred. No. 3.5e-73;
Matches 205; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 VNITSPVRLIHGTGKSGALLSVQSSSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 60
DB 34 VNITSPVRLIHGTGKSGALLSVQSSSTSDRPVVKWQKRDKPVTVVQSIGTEVIGTLRP 93
QY 61 DYDRIRLFENGSLLSLDLQADSGTYEVEISITDDTFTGKKTINLTVDVPISRPQVLVA 120
DB 94 DYDRIRLFENGSLLSLDLQADSGTYEVEISITDDTFTGKKTINLTVDVPISRPQVLVA 153
QY 121 STTVLESEAFTLNCSHENGTPKSYTWLKGKPLNDSRMLLSPDQKVLITITRVLMEDDD 180
DB 154 STTVLESEAFTLNCSHENGTPKSYTWLKGKPLNDSRMLLSPDQKVLITITRVLMEDDD 213
QY 181 LYSCWVENPISQGRSLPVKITVYRRSS 207
DB 214 LYSCWVENPISQGRSLPVKITVYRRSS 240
RESULT 4
Q640R3 PRELIMINARY; PRT; 413 AA.
ID Q640R3
AC Q640R3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 2900042E01Rik protein (Fragment).
GN Name=2900042E01Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=C57BL/6; TISSUE=Brain;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Hulton E., Kettman M., Madan A.C., Shevchenko Y., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywinski M.I., Skaleck U., Smailus D.E., Schnerch A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;

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RA Director MGC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC082537; AA082537.1; --
FT NON_TER 1
SQ SEQUENCE 413 AA; 45665 MW; B6EFA2D6D2CA3C1 CRC64;

Query Match 98.5%; Score 1029; DB 2; Length 413;
Best Local Similarity 98.6%; Pred. No. 7e-73;
Matches 204; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNITSPVRLIHGTGKSAALLSVQYSTSDSRPVVKWQLKRPVTVVQSIGTEVIGTLRP 60
DB 29 VNITSPVRLIHGTGKSAALLSVQYSTSDSRPVVKWQLKRPVTVVQSIGTEVIGTLRP 88
QY 61 DYDRIRLRFENGSLLSLDLQADEGTYEVEISITDDTGTGKTNLTVDVPISRPQVLA 120
DB 89 DYDRIRLRFENGSLLSLDLQADEGTYEVEISITDDTGTGKTNLTVDVPISRPQVLA 148
QY 121 STTVLESEAFNLCSHENGTKPSYTLWKDGKPLNDSRMLLSPDKVLTITRVLMEDD 180
DB 149 STTVLESEAFNLCSHENGTKPSYTLWKDGKPLNDSRMLLSPDKVLTITRVLMEDD 208
QY 181 LYSVMENPISQGRSLPVKITVYRRSS 207
DB 209 LYSVMENPISQGRSLPVKITVYRRSS 235

RESULT 5

Q6UX10 PRELIMINARY; PRT; 450 AA.
AC Q6UX10;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE WLKV305.
GN ORFNames=UNQ305;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yanaura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;

RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment";
RL Genome Res. 13:2265-2270(2003).

DR EMBL: AY358345; AAQ88711.1; --
DR InterPro; IPR003599; IG-
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; Ig 1.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 450 AA; 50114 MW; A22FF822CC3CB226 CRC64;

Query Match 25.6%; Score 268; DB 2; Length 450;
Best Local Similarity 31.9%; Pred. No. 7.3e-13;
Matches 67; Conservative 43; Mismatches 90; Indels 10; Gaps 7;

QY 1 VNITSPVRLIHGTGKSAALLSVQYSTSDSRPVVKWQLKRPVTVVQSIGTEVIG 56
DB 20 LKVTVPSTHVGVRGQALYLPVHYGFHTPASDIQII-WLFRPHTMPKYLKSVKSVVP 78

QY 57 TLRPDYDRIRLRF-ENGSLLSLDLQADEGTYEVEISIT-DDTGTGKTNLTVDVPISR 114
DB 79 DL--EYQHKFTMPNPASLLINPLQFPDEGNYIVKVNIOGNGTLSASOKIQVTVDPPVTK 136
QY 115 PQVLV-ASTTVLESEAFNLCSHENGTKPSYTLWKDGKPLNDSRMLLSPDKVLTITR 173
DB 137 PVQIHPPSGAVEVVGWNTLTCHVEGTRLAYQMLKNGRPVHTSTSYFSQNNTLHIAP 196
QY 174 VLMEDDDLSCVMENPISQGRSLPVKITVY 203
DB 197 VTREDIGNYSCLVRNPVSEMSDIIMPIIY 226

RESULT 6

Q99232 PRELIMINARY; PRT; 278 AA.
AC Q99232;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Carcinoembryonic antigen family member protein precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CD-1; TISSUE=Colon;
RX MEDLINE=91093141; PubMed=1985902;
RA Turbide C., Rojas M., Stanners C.P., Beauchemin N.;
RT "A mouse carcinoembryonic antigen gene family member is a calcium-
RT dependent cell adhesion molecule.";
RL J. Biol. Chem. 266:309-315(1991).
DR EMBL: X53084; CAA37251.1; --
DR PIR; A39037; A39037.
DR PIR; JCI506; JCI506.
DR HSSP; Q61353; 1L6Z.
DR MGD; MGI:1347245; Ceacam1.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; Ig 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Signal.
FT SIGNAL 1 34 Potential.
FT CHAIN 35 278 Potential.
SQ SEQUENCE 278 AA; 29943 MW; 1A9CEBF18770258C CRC64;

Query Match 19.4%; Score 202.5; DB 2; Length 278;
Best Local Similarity 32.1%; Pred. No. 5.9e-08;
Matches 54; Conservative 31; Mismatches 74; Indels 9; Gaps 5;

QY 40 RDEPVTYVQSIGTEVIGTLR----PYDRIRLRFENGSLLSLDLQADEGTYEVEISITD 95
DB 69 KGNPVSTNAEIVHVFVTGNTTTPGPAHSGRETGVYVNGSLLIQRTVTKDTGVYTIIE--MTD 126
QY 96 DTF-TGKTNLTVDVPISRPQVLAFTVLESEAFNLCSHENGTKPSYTLWKDGKPL 154
DB 127 ENFRTEATVQFHVHQPVTQPSLQVNTTNTVKEL-DSVTLTCL-SNDIGANTQLNFSQSL 184
QY 155 LNDSRMLLSPDKVLTITRVLMEDDDLSCVMENPISQGRSLPVKITV 202
DB 185 QLTERMTLSQNNILRIDPIKREDAGEYQCEISNPVSVKRSNSIKLOI 232

RESULT 7

Q61354 PRELIMINARY; PRT; 341 AA.
AC Q61354;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

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DE Biliary glycoprotein precursor.
GN Name=Ceacam1, Synonyms=Bgph;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3D1; TISSUE=Colon;
RA MEDLINE=93273228; PubMed=8500759; DOI=10.1016/0378-1119(93)90716-G;
RX McCuaig K., Rosenberg M., Turbide C., Beauchemin N., Nedellec P.;
RT "Expression of the Bgp gene and characterization of mouse colon
biliary glycoprotein isoforms.";
RL Gene 127:173-183(1993).
DR EMBL; X67283; CAA47700.1; -.
DR PIR; JC1512; JC1512.
DR HSP; G61353; IL62.
DR MGD; MGI:1347245; Ceacam1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW SIGNAL.
FT SIGNAL
FT SIGNAL
SQ SEQUENCE 341 AA; 36901 MW; B5278D6606996341 CRC64;

Query Match 19.4%; Score 202.5; DB 2; Length 341;
Best Local Similarity 32.1%; Pred. No. 7.6e-08;
Matches 54; Conservative 31; Mismatches 74; Indels 9; Gaps 5;

QY 40 RDKPTVVQSIGTGVICTLR-----PDYRDRIRLPENGSLLSDLQLADEGTYEVEISITD 95
DB :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 126
69 KGNPVSTNAEIVHVTGNTKTTTTPAHSGRVTSNGSLLIQRTVTVKDTGVYTIE--MTD 126

QY 96 DTF-TGKNTINLTVDVPISRPQVLVASTVTLSEAFATLNCSHENGKPSVTMLKDGKPL 154
DB :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 184
127 ENFRTEATQVHVHPQVPSLQVNTVTKEL-DSVTLTCL-SNDIGANIQLMFLNSQSL 184

QY 155 LNSRMLSPQKQVLTTRVLMEDDDLVSCMVENPISQGRSLPVKITV 202
DB :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 232
185 QLTERMTLSQNSILRIDPIKREDAGEYQCEISNPVSVKRSNSIKLDI 232

RESULT 8
Q6UY47 PRELIMINARY; PRT; 292 AA.
AC Q6UY47;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CEACAM3.
GN ORFNames=UNQ3098;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=2287296; PubMed=12975309; DOI=10.1101/gr.1293003;
RX Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbe E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wileand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).

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DR EMBL; AY358084; AAQ88451.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 292 AA; 32315 MW; 2D4DE7851E301C57 CRC64;

Query Match 18.1%; Score 189.5; DB 2; Length 292;
Best Local Similarity 31.2%; Pred. No. 6.7e-07;
Matches 60; Conservative 33; Mismatches 88; Indels 11; Gaps 6;

QY 15 GKSAALLSVQYSSSTSDRPVVKWLKDKDPVTVVQSIGTEVIGT-LR---PDYRDRIRLFE 70
DB :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 103
48 GENVHLSVVVLPEN----LYSYGWYKGTVEPNQLIAAYVIDTHVTPGPAYSGRETISP 103

QY 71 NGSLLLSDLQLADEGTYEVEISITDFTTGEKNTINLTVDVPISRPQVLVASTVTLSE 130
DB :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 161
104 SGLHFQNVLTEDTGYNQLQVTVNSQIE-QASHHLRVVESVAQPSIQASSTVTE-KGS 161

QY 131 FTLNCSHENGKPSVTMLKDGKPLNDSRLMLSPDQKVLTTITRLVMEDDDLVSCMVENPI 190
DB :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 220
162 VVLTLC-HTNNTGTSFQWIFNNQLQVTKRMKLSWFNHVLITDPIQEDAGEYQCEVSNPV 220

QY 191 SQGRSLPVKITV 202
DB :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 232
221 SSNRSDPLKLTV 232

RESULT 9
Q75296 PRELIMINARY; PRT; 235 AA.
AC Q75296;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE R29124_1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,
RA Dangnanan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
RA Kobayashi A., Olsen A.S., Carrano A.V.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005626; AAC34569.1; -.
DR HSP; G61353; IL62.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 235 AA; 26415 MW; 8E499BF68D884BFB CRC64;

Query Match 17.8%; Score 185.5; DB 2; Length 235;
Best Local Similarity 30.7%; Pred. No. 1.1e-06;
Matches 59; Conservative 34; Mismatches 88; Indels 11; Gaps 6;

QY 15 GKSAALLSVQYSSSTSDRPVVKWLKDKDPVTVVQSIGTEVIGT-LR---PDYRDRIRLFE 70
DB :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 103
48 GENVHLSVVVLPEN----LYSYGWYKGTVEPNQLIAAYVIDTHVTPGPAYSGRETISP 103

QY 71 NGSLLLSDLQLADEGTYEVEISITDFTTGEKNTINLTVDVPISRPQVLVASTVTLSE 130
DB :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 161
104 SGLHFQNVLTEDTGYNQLQVTVNSQIE-QASHHLRVVESVAQPSIQASSTVTE-KGS 161

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Db 104 SGLHFQNVLTEDTGYTLQVTRNSQIE-QASHHLRVVESAQSIQASSTVTVE-KGS 161
Qy 131 FTLCNCHENGKPSYTWLKGKPLANDSRMLSPDQKVLITRVLMDLDDLYSCWVENPI 190
Db 162 VLITC-HYNTGTSTQFQWIFNNQRLQVTRKMLSLWFNHLMTIDPIRQEDAGEYQCEVSNPV 220
Qy 191 SQGRSLPVKITV 202
Db 221 SSNSRDPKLTV 232

RESULT 10
Q61351 PRELIMINARY; PRT; 458 AA.
AC Q61351
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Biliary glycoprotein precursor.
GN Name=Ceacam1; Synonyms=Bgpe;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD1; TISSUE=Colon;
RX MEDLINE=93273228; PubMed=8500759; DOI=10.1016/0378-1119(93)90716-G;
RA McCuaig K., Rosenberg M., Turbide C., Beauchemin N., Nedellec P.;
RT "Expression of the Bgp gene and characterization of mouse colon
biliary glycoprotein isoforms.";
RL Gene 127:173-183(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CD1; TISSUE=Colon;
RX Huang D.C., Huang X.F., Novel M., Novel G.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; X67281; CAA47698.1; -.
DR PIR; S34338; S34338.
DR HSSP; Q61353; 1L6Z.
DR MGD; MGI:1347245; Ceacam1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS00835; IG_LIKE; 3.
KW Signal.
FT SIGNAL 1 34 Potential.
SQ SEQUENCE 458 AA; 49671 MW; 1DC61FFCD875B85F CRC64;
Query Match 17.3%; Score 181; DB 2; Length 458;
Best Local Similarity 27.8%; Pred. No. 5.3e-06;
Matches 47; Conservative 34; Mismatches 80; Indels 8; Gaps 4;
Qy 40 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLPENGSLLSLDLQLADEGTYVEISITD 95
Db 69 KGNPVSTNAEIVHFVTGNTKTTGPAHSGRETIVYNSGSLLIQRTVTKDTGYTIE--MTD 126
Qy 96 DTF-TGEKTNLTVDVPIRSRQVLVASTTVLELSEAFITNC-SHENGTKPSYTWLKGK 153
Db 127 ENFRTEATVQFHVHQLLKPNITSNNSNPVEGDSVSLTCDSYTDPDNIYLSRNGES 186
Qy 154 LLNDSRMLLSPDQKVLITRVLMDLDDLYSCWVENPISQGRSLPVKITV 202
Db 187 LSEGDRLKLSGNRTLTLLNTRNDTGPYVCETRNVPVSNRSDPPFSLNI 235

RESULT 11
Q61352 PRELIMINARY; PRT; 521 AA.
AC Q61352
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Biliary glycoprotein precursor.
GN Name=Ceacam1; Synonyms=Bgpt;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD1; TISSUE=Colon;
RX MEDLINE=93273228; PubMed=8500759; DOI=10.1016/0378-1119(93)90716-G;
RA McCuaig K., Rosenberg M., Turbide C., Beauchemin N., Nedellec P.;
RT "Expression of the Bgp gene and characterization of mouse colon
biliary glycoprotein isoforms.";
RL Gene 127:173-183(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CD1; TISSUE=Colon;
RX Huang D.C., Huang X.F., Novel M., Novel G.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; X67281; CAA47698.1; -.
DR PIR; S34338; S34338.
DR HSSP; Q61353; 1L6Z.
DR MGD; MGI:1347245; Ceacam1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS00835; IG_LIKE; 3.
KW Signal.
FT SIGNAL 1 34 Potential.
SQ SEQUENCE 521 AA; 56630 MW; 566DFEB9F2P87FCD CRC64;
Query Match 17.3%; Score 181; DB 2; Length 521;
Best Local Similarity 27.8%; Pred. No. 6.2e-06;
Matches 47; Conservative 34; Mismatches 80; Indels 8; Gaps 4;
Qy 40 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLPENGSLLSLDLQLADEGTYVEISITD 95
Db 69 KGNPVSTNAEIVHFVTGNTKTTGPAHSGRETIVYNSGSLLIQRTVTKDTGYTIE--MTD 126
Qy 96 DTF-TGEKTNLTVDVPIRSRQVLVASTTVLELSEAFITNC-SHENGTKPSYTWLKGK 153
Db 127 ENFRTEATVQFHVHQLLKPNITSNNSNPVEGDSVSLTCDSYTDPDNIYLSRNGES 186
Qy 154 LLNDSRMLLSPDQKVLITRVLMDLDDLYSCWVENPISQGRSLPVKITV 202
Db 187 LSEGDRLKLSGNRTLTLLNTRNDTGPYVCETRNVPVSNRSDPPFSLNI 235

RESULT 12
Q8C9E4 PRELIMINARY; PRT; 538 AA.
AC Q8C9E4
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
library, clone:A630078M16 product:lymphocyte antigen 9, full insert
sequence. (Fragment).
GN Name=Ly9;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
```



```
QY 124 VLEL-SEAFITLNCSENGTKPS--YTWLKGKPLINDSRMLLSPDQKVLTTITRVLMEDDD 180
Db 157 PSDTSCFTLICT-VKGTQDSVQVSWTRE-----DTHLNTYDGSHTLRVSQSVCDPDL 209
QY 181 LYSCHVENPISQGRSLPVKI 200
Db 210 PYTCKAWNPVSNSSQPVRI 229

RESULT 14
Q7TMP7 PRELIMINARY; PRT; 649 AA.
ID Q7TMP7
AC Q01965; Q9ES29; Q9ES35; Q9ES36; PRT; 654 AA.
DT 01-OCT-2003 (TREMELrel. 25, Created)
DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Ly9 protein (Fragment).
GN Name=Ly9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A. TISSUE=Hematopoietic Stem Cell;
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.;
RA Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055380; AAH5380.1; -.
DR HSP; P08921; IHHG.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS00835; IG LIKE; 2.
FT NON TER
SQ SEQUENCE 649 AA; 72414 MW; AD6A09381C063B34 CRC64;

Query Match 17.3%; Score 180.5; DB 2; Length 649;
Best Local Similarity 27.5%; Pred. No. 8.9e-06;
Matches 55; Conservative 40; Mismatches 90; Indels 15; Gaps 7;

QY 5 SPVRLHGTCKSALLSVQVSTSDRPVVKWQKLRKDPVTVVQSIGTEVIGTLRPDYRD 64
Db 45 TPPTVISMGLGCVTFSLNISRKAEIHII-WNC---PPKALALVYFKKRIITLDKGYNG 100
QY 65 RIRLPENG-SULLSDQLADEGTVEVEISITDDTFTGTEKTNLTAVDVPISRPQVLVASTT 123
```

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Db 101 RLKVEDGYSLYMNLTKSDSGSYHAQINQKNVILTTNKEFTLHIYEKLPQIIVESVT 160
QY 124 VLEL-SEAFITLNCSENGTKPS--YTWLKGKPLINDSRMLLSPDQKVLTTITRVLMEDDD 180
Db 161 PSDTSCFTLICT-VKGTQDSVQVSWTRE-----DTHLNTYDGSHTLRVSQSVCDPDL 213
QY 181 LYSCHVENPISQGRSLPVKI 200
Db 214 PYTCKAWNPVSNSSQPVRI 233

RESULT 15
LY9_MOUSE
ID LY9_MOUSE STANDARD; PRT; 654 AA.
AC Q01965; Q9ES29; Q9ES35; Q9ES36;
DT 01-JUN-1994 (Rel. 29, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE T-lymphocyte surface antigen Ly-9 precursor (lymphocyte antigen 9)
DE (Cell-surface molecule Ly-9).
GN Name=Ly9; Synonyms=Ly-9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A. AND POLYMORPHISM.
RC STRAIN=129/SV, BALB/c, and C57BL/6; TISSUE=Spleen;
RX MEDLINE=20424510; PubMed=10970093; DOI=10.1007/s002510000209;
RA Tovar V., de la Fuente M.A., Pizcueta P., Bosch J., Engel P.;
RT "Gene structure of the mouse leukocyte cell surface molecule Ly9.";
RL Immunogenetics 51:788-793 (2000).
RN [2]
SEQUENCE OF 22-654 FROM N.A., AND SEQUENCE OF 48-59.
RX MEDLINE=92373003; PubMed=1506686;
RA Sandrin M.S., Gumley T.P., Henning M.M., Vaughan H.A., Genez L.J.,
RA Trapani J.A., McKenzie I.F.C.;
RT "Isolation and characterization of cDNA clones for mouse Ly-9.";
RL J. Immunol. 149:1636-1641 (1992).
CC -! FUNCTION: May participate in adhesion reactions between T
CC lymphocytes and accessory cells by homophilic interaction.
CC -! SUBCELLULAR LOCATION: Type I membrane protein.
CC -! TISSUE SPECIFICITY: Lymphocytes.
CC -! SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -! SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF244131; AAG14997.1; -.
DR EMBL; AF244130; AAG14996.1; -.
DR EMBL; AF246701; AAG13268.2; -.
DR EMBL; AF245117; AAG13268.2; JOINED.
DR EMBL; AF245506; AAG13268.2; JOINED.
DR EMBL; AF245118; AAG13268.2; JOINED.
DR EMBL; AF245507; AAG13268.2; JOINED.
DR EMBL; AF245508; AAG13268.2; JOINED.
DR EMBL; AF245509; AAG13268.2; JOINED.
DR EMBL; AF245510; AAG13268.2; JOINED.
DR EMBL; AF246699; AAG13268.2; JOINED.
DR EMBL; AF246700; AAG13268.2; JOINED.
DR EMBL; M84412; AAA39468.1; -.
DR HSP; P08921; IHHG.
DR MGD; MGI:96885; Ly9.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
```

Wed Jul 27 09:56:17 2005

DR PROSITE; P550835; IG LIKE; 2.
KW Antigen; Cell adhesion; Direct protein sequencing; Glycoprotein;
KW Immunoglobulin domain; Polymorphism; Repeat; Signal; Transmembrane.
FT SIGNAL 1 47

FT	1	T-lymphocyte surface antigen Ly-9.
FT	47	Extracellular (Potential).
FT	48	CHAIN
FT	654	DOMAIN
FT	48	CHAIN
FT	453	DOMAIN

FT	DOMAIN	475	Cytoplasmic (Potential).
FT	TRANSMEM	454	Potential.
FT	DOMAIN	474	Potential.
FT	DOMAIN	475	Cytoplasmic (Potential).

FT	DOMAIN	48	Ig-like V-type 1.
FT	DOMAIN	159	Ig-like C2-type 1.

1	DOMAIN	250	Ig-like V-type 2.
FT	DOMAIN	250	Ig-like V-type 2.
FT	DOMAIN	353	Ig-like C2-type 2.

FT	DISULFID	172	242	Potential.
FT	DISULFID	178	222	Potential.

11	DISULFID	270	Potential.
FT	DISULFID	376	Potential.
FT	DISULFID	382	Potential.

1	FT	CARBOHYD	68	N-linked (GLcNAc. . .)	(Potential).
2	FT	CARBOHYD	120	N-linked (GLcNAc. . .)	(Potential).

229	linked (GlcNAc. . .)	(Potential).
231	N-linked (GlcNAc. . .)	(Potential).
284	N-linked (GlcNAc. . .)	(Potential).
284	N-linked (GlcNAc. . .)	(Potential).

FT	CARBOHYD	201	N-linked (GlcNAc. . .)	(Potential)
FT	CARBOHYD	390	N-linked (GlcNAc. . .)	(Potential)
FT	CARBOHYD	412	N-linked (GlcNAc. . .)	(Potential)

FT	CARBOHYD	412	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	423	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	434	N-linked (GlcNAc. . .)	(Potential).

	CARDINAL	D -> G (in Ly9-1).	10	10
FT	VARIANT	G -> S (in Ly9-1).	14	14

21	VARIANT	79	O -> T (in Ly9-1).
22	VARIANT	79	O -> T (in Ly9-1).
23	VARIANT	91	F -> S (in Ly9-1).

FT	130	H -> Y (in Ly9-1).
FT	139	I -> T (in Ly9-1).

FT	366	P → S.
VARIANT	362	
FT	366	K → N (in Ly9-1).
VARIANT	366	

	VARIANT	550
FT	E -> K (in Ly9-1).	550
FT	M -> I (in Ly9-1).	550

VARIANT	283
FT CONFLICT	283
G -> E (in Ly9-1).	592
F -> L (in Ref. 2).	283

FT	CONFLICT	499	T -> P (in Ref. 2).
FT	CONFLICT	560	V -> L (in Ref. 2).

FT	647	CONFLICT	654	TPTYENFT -> SPYL (in Ref. 2).
SQ	654	SEQUENCE	654	AA; 73142 MW; 1CBEE99708AE8EE7 CRC64;

Query Match 17.3%; Score 180.5; DB 1; Length 654;

Best Local Similarity 27.5%; Pred. No. 9e-06;
Matches 55; Conservative 40; Mismatches 90; Indels 15;

QY 5 SPVRLIHGTGKSAALLSVQYSSTSSDRPVPVKWQLKRDKPVTVVQSIGTEVIGTLR

[illegible]

QY 65 RIRLFENG-SLLSDDLQLADEGTYEVEISITDDDTFTGKTNLTVDVPISRQVLT

Db 106 RLVSEGDGYSLYMSNLTKSDSGSYHAQINQKVILTTNKFTLHIYEKLOKQPII

QY 124 VLEL-SEAFITLNCSENGTKPS--YTWLKDCKPLINDSRMLLSPDQKVLITITRVL

Db 166 PSDDTDCSTFTLLCT-VKGTKDSVQYSWTRE-----DTHLNTYDGSHTLRVSQSV

QY 181 LYSCMVENPISQGRSLPVKI 200

219 PYTCKAWNPVSNSSQPVR I 238

Search completed: July 26, 2005, 16:13:00
Job time : 53.996 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 15:54:21 ; Search time 117.856 Seconds
(without alignments)
1365.166 Million cell updates/sec

Title: US-10-706-691-16

Perfect score: 2122

Sequence: 1 MKRRGALSRASRLRLAPP.....TAGVHIIRQDEAGPVEISA 416

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2122	100.0	416	7	Abg75379 Predicted
2	2122	100.0	416	7	Abg75377 Human INS
3	2122	100.0	416	8	Ado47892 Human pro
4	2122	100.0	416	8	Adsl1056 Human the
5	1992	93.9	418	7	Abg75378 Murine IN
6	1962	92.5	383	8	Ado47895 Human mat
7	1478.5	69.7	367	8	Adg65357 Novel hum
8	1472	69.4	298	5	Aae14784 Human imm
9	1352	63.7	270	8	Ado47887 Human pro
10	1352	63.7	270	8	Adsl1055 Human the
11	1205	56.8	246	7	Abg75380 INSP052 e
12	1192	56.2	237	8	Ado47890 Human tra
13	1189	56.0	256	8	Adm87341 Human pro
14	1178	55.5	256	4	Aam24238 Human EST
15	1178	55.5	256	8	Adm87787 Human EST
16	1178	55.5	256	8	Adsl12269 Human the
17	1178	55.5	256	8	Adsl12268 Human the
18	1157	54.5	224	5	Aae26421 Human tra
19	570	26.9	114	7	Abg75371 Human INS
20	522	24.6	100	7	Abg75376 Human INS
21	484	22.8	188	7	Abg75372 Human INS
22	282	13.3	338	4	Aam78339 Human pro
23	282	13.3	450	2	Aay13398 Amino aci
24	282	13.3	450	3	Adc78632 Human PRO
25	282	13.3	450	4	Aab80266 Human PRO

ALIGNMENTS

RESULT 1

ABG75379
ID ABG75379 standard; protein; 416 AA.

XX AC ABG75379;

DT 22-APR-2004 (first entry)

DE Predicted INSP052 protein.

XX

INSP052; human; cell proliferation; autoimmune disease; inflammation; cardiovascular disease; neurological disease; psychiatric disease; developmental disease; metabolic disorder; infection; immunoglobulin domain-containing cell surface recognition molecule.

XX Unidentified.

OS WO2003093316-A2.

PN 13-NOV-2003.

PD 30-APR-2003; 2003WO-GB001851.

XX 30-APR-2002; 2002GB-00009884.

PR (ARES-) ARES TRADING SA.

XX Davids AR, Fagan RJ, Phelps CB, Power C;

XX WPI; 2003-903655/82.

DR N-PSDB; ACH01277.

XX New INSP052 polypeptides and nucleic acids, useful in diagnosing and treating cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, psychiatric, developmental, genetic or metabolic disorder.

XX Example 2; Fig 5; Opp; English.

CC The present invention provides the protein and coding sequences of a novel human immunoglobulin domain-containing cell surface recognition molecule known as INSP052. The polypeptide is useful as immunoglobulin domain-containing cell surface recognition molecule. The sequences may also be used in therapy or diagnosing a disease or in the manufacture of a medicament for treating a disease. The disease is a cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, psychiatric, developmental, genetic or metabolic disorder, an infection or other pathological condition. The polypeptides and nucleic acids are essential to the structural integrity and homeostatic functioning of most tissues.

Aau12360 Human PRO
Aau81958 Human PRO
Abu71644 Human PRO
Abo17804 Novel hum
Abu71499 Human PRO
Abu81058 Human PRO
Abu71945 Human sec
Abo01828 Novel hum
Abo66758 Human PRO
Abo54401 Human sec
Abo47416 Human sec
Abu59839 Novel sec
Abo25029 Human sec
Abo64553 Human sec
Abo67399 Human sec
Abo14919 Human sec
Abu67034 Human sec
Abu69676 Novel hum
Abo14858 Human sec
Ada45897 Novel hum

26 282 13.3 450 4 AAU12360
27 282 13.3 450 5 AAU81958
28 282 13.3 450 6 ABU71644
29 282 13.3 450 6 ABO17804
30 282 13.3 450 6 ABU71499
31 282 13.3 450 6 ABU81058
32 282 13.3 450 6 ABU71945
33 282 13.3 450 6 ABO01828
34 282 13.3 450 6 ABO66758
35 282 13.3 450 6 ABO54401
36 282 13.3 450 6 ABO47416
37 282 13.3 450 6 ABU59839
38 282 13.3 450 6 ABO25029
39 282 13.3 450 6 ABU64553
40 282 13.3 450 6 ABU67399
41 282 13.3 450 6 ABO14919
42 282 13.3 450 6 ABU67034
43 282 13.3 450 6 ABU69676
44 282 13.3 450 6 ABO14858
45 282 13.3 450 6 ADA45897

CC The present sequence is a polypeptide shown in the invention

XX Sequence 416 AA;

Query Match 100.0%; Score 2122; DB 7; Length 416;
 Best Local Similarity 100.0%; Pred. No. 2.4e-146;
 Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKRERGALSRRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTGKSALLSVQYSST 60
 Db 1 MKRERGALSRRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTGKSALLSVQYSST 60

Qy 61 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYPDRIRLRFENGSLLLSDQLADEGTY 120
 Db 61 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYPDRIRLRFENGSLLLSDQLADEGTY 120

Qy 121 EVEISITDDTFTGKTNLTVDVPISRPQVLVASTTVLELSEAFITLNCSEHNGTKPSYTW 180
 Db 121 EVEISITDDTFTGKTNLTVDVPISRPQVLVASTTVLELSEAFITLNCSEHNGTKPSYTW 180

Qy 181 LKDGKPLNDSRMLLSPDQKVLITRVLMEDDDLVSCWENPISQGRSLPVKITVYRRSS 240
 Db 181 LKDGKPLNDSRMLLSPDQKVLITRVLMEDDDLVSCWENPISQGRSLPVKITVYRRSS 240

Qy 241 LYIILSTGGIFLLVTLVTVACWKPKRKQKLEKQNSLEYMDQNDRLKPEADTLPRSG 300
 Db 241 LYIILSTGGIFLLVTLVTVACWKPKRKQKLEKQNSLEYMDQNDRLKPEADTLPRSG 300

Qy 301 EQERKNPMALYILKDKDSPETEENPAPEPRSATPPGPGYSVPVPGSPGLPIRSARR 360
 Db 301 EQERKNPMALYILKDKDSPETEENPAPEPRSATPPGPGYSVPVPGSPGLPIRSARR 360

Qy 361 YPRSPARSPATGRTHSSPPRAPSPGSRSSASRTLRAGVHIIREQDEAGPVEISA 416
 Db 361 YPRSPARSPATGRTHSSPPRAPSPGSRSSASRTLRAGVHIIREQDEAGPVEISA 416

RESULT 2

ABG75377
 ID ABG75377 standard; protein; 416 AA.
 AC AC
 AC ABG75377;
 DT 22-APR-2004 (first entry)
 XX Human INSP052 complete protein.
 XX INSP052; human; cell proliferation; autoimmune disease; inflammation;
 KW cardiovascular disease; neurological disease; psychiatric disease;
 KW developmental disease; metabolic disorder; infection;
 KW immunoglobulin domain-containing cell surface recognition molecule.
 XX OS
 XX Homo sapiens.
 XX WO2003093316-A2.
 XX PD 13-NOV-2003.
 XX PF 30-APR-2003; 2003WO-GB001851.
 XX PR 30-APR-2002; 2002GB-00009884.
 XX XX (ARES-) ARES TRADING SA.
 XX PI Davids AR, Fagan RJ, Phelps CB, Power C;
 XX DR WPI; 2003-903655/82.
 XX DR N-PSDB; ACH01275.
 XX FT New INSP052 polypeptides and nucleic acids, useful in diagnosing and
 PT treating cell proliferative, autoimmune/inflammatory, cardiovascular,
 PT neurological, psychiatric, developmental, genetic or metabolic disorder.
 XX XX

PS Claim 1; Page 67; Opp; English.

XX The present invention provides the protein and coding sequences of a novel human immunoglobulin domain-containing cell surface recognition molecule known as INSP052. The polypeptide is useful as immunoglobulin domain-containing cell surface recognition molecule. The sequences may also be used in therapy or diagnosing a disease or in the manufacture of a medicament for treating a disease. The disease is a cell proliferative, CC autoimmune/inflammatory, cardiovascular, neurological, psychiatric, CC developmental, genetic or metabolic disorder, an infection or other CC pathological condition. The polypeptides and nucleic acids are essential CC to the structural integrity and homeostatic functioning of most tissues. CC The present sequence is a polypeptide shown in the invention

XX Sequence 416 AA;

Query Match 100.0%; Score 2122; DB 7; Length 416;
 Best Local Similarity 100.0%; Pred. No. 2.4e-146;
 Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKRERGALSRRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTGKSALLSVQYSST 60
 Db 1 MKRERGALSRRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTGKSALLSVQYSST 60

Qy 61 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYPDRIRLRFENGSLLLSDQLADEGTY 120
 Db 61 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYPDRIRLRFENGSLLLSDQLADEGTY 120

Qy 121 EVEISITDDTFTGKTNLTVDVPISRPQVLVASTTVLELSEAFITLNCSEHNGTKPSYTW 180
 Db 121 EVEISITDDTFTGKTNLTVDVPISRPQVLVASTTVLELSEAFITLNCSEHNGTKPSYTW 180

Qy 181 LKDGKPLNDSRMLLSPDQKVLITRVLMEDDDLVSCWENPISQGRSLPVKITVYRRSS 240
 Db 181 LKDGKPLNDSRMLLSPDQKVLITRVLMEDDDLVSCWENPISQGRSLPVKITVYRRSS 240

Qy 241 LYIILSTGGIFLLVTLVTVACWKPKRKQKLEKQNSLEYMDQNDRLKPEADTLPRSG 300
 Db 241 LYIILSTGGIFLLVTLVTVACWKPKRKQKLEKQNSLEYMDQNDRLKPEADTLPRSG 300

Qy 301 EQERKNPMALYILKDKDSPETEENPAPEPRSATPPGPGYSVPVPGSPGLPIRSARR 360
 Db 301 EQERKNPMALYILKDKDSPETEENPAPEPRSATPPGPGYSVPVPGSPGLPIRSARR 360

Qy 361 YPRSPARSPATGRTHSSPPRAPSPGSRSSASRTLRAGVHIIREQDEAGPVEISA 416
 Db 361 YPRSPARSPATGRTHSSPPRAPSPGSRSSASRTLRAGVHIIREQDEAGPVEISA 416

RESULT 3

ADO47892
 ID ADO47892 standard; protein; 416 AA.
 AC AC
 AC ADO47892;
 DT 15-JUL-2004 (first entry)
 XX Human protein SEQ ID NO:9.
 XX human; virucide; anti-HIV; cytostatic; antiinflammatory; antiallergic;
 KW immunosuppressive; antiarteriosclerotic; hypotensive; osteopathic;
 KW antianaemic; neuroprotective; nootropic; antiparkinsonian; antiasthmatic;
 KW haemostatic; antidiabetic; cardiant; HIV; viral infection; cancer;
 KW inflammation; allergy; graft rejection; atherosclerosis; hypertension;
 KW osteoporosis; anaemia; Alzheimer's disease; Parkinson's disease; asthma;
 KW diabetes; myocardial infarction; haemophilia.
 XX OS
 XX Homo sapiens.
 XX WO2004007672-A2.
 XX PD 22-JAN-2004.
 XX XX

PF 09-JUL-2003; 2003WO-US021703.
 XX
 PR 12-JUL-2002; 2002US-0395402P.
 XX
 PA (NUVE-) NUVELO INC.
 XX
 PI Rupp F, Wang J, Zhou P, Wehrman T, Wang ZW, Tang YT;
 XX WPI; 2004-122914/12.
 DR N-PSDB; ADO47891.
 XX
 PT New isolated polypeptides and polynucleotides useful in diagnostics,
 PT forensics, in preventing or treating diseases such as HIV and cancer, and
 PT as drug targets.
 XX
 PS Claim 10; SEQ ID NO 9; 205pp; English.
 XX
 CC The invention relates to novel isolated polynucleotides and polypeptides
 CC encoded by them. Also included are mutants or variants of the
 CC polynucleotides and polypeptides. A polypeptide of the invention has
 CC virucide, anti-HIV, cytostatic, antiinflammatory, antiallergic,
 CC immunosuppressive, antiarteriosclerotic, hypotensive, osteopathic,
 CC antianaemic, neuroprotective, nootropic, antiparkinsonian, antiaschmatic,
 CC haemostatic, antidiabetic, and cardiant activity. The composition and
 CC methods are useful in diagnostics, forensics, gene or chromosome mapping,
 CC identification of mutations responsible for genetic disorders or other
 CC traits, in assessing biodiversity, or in producing many other types of
 CC data and products dependent on DNA and amino acid sequences. They may
 CC also be used in preventing or treating diseases (e.g. HIV and other viral
 CC infections, cancer, inflammation, allergies, graft rejection,
 CC atherosclerosis, hypertension, osteoporosis, anaemia, Alzheimer's
 CC disease, Parkinson's disease, asthma, diabetes, myocardial infarction or
 CC haemophilia). They may also be used as targets in drug screening. The
 CC present sequence represents a polypeptide of the invention.
 XX
 SQ Sequence 416 AA;
 Query Match 100.0%; Score 2122; DB 8; Length 416;
 Best Local Similarity 100.0%; Pred. No. 2.4e-146;
 Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKRERGALSASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTGKSAALLSVQYSST 60
 DB 1 MKRERGALSASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTGKSAALLSVQYSST 60
 QY 61 SSDRPVVKWQLKRDKPVTWQSIGTEVIGTLRPDYDRIRLRFENGSLLLSDQLADEGTY 120
 DB 61 SSDRPVVKWQLKRDKPVTWQSIGTEVIGTLRPDYDRIRLRFENGSLLLSDQLADEGTY 120
 QY 121 EVEISITDDTFTGKTNLTVDVPISRPQVLVASTTTLSEAFTLNCSHENGTKPSYTW 180
 DB 121 EVEISITDDTFTGKTNLTVDVPISRPQVLVASTTTLSEAFTLNCSHENGTKPSYTW 180
 QY 181 LKDGKPLNDSRMLLSPDKQLTITRVLMEDDDLKQNSLEYMDNDRLKPEADTLPRSG 240
 DB 181 LKDGKPLNDSRMLLSPDKQLTITRVLMEDDDLKQNSLEYMDNDRLKPEADTLPRSG 240
 QY 241 LYIILSTGGIFLLVTLTVCAWPKSRKQKLEKQNSLEYMDNDRLKPEADTLPRSG 300
 DB 241 LYIILSTGGIFLLVTLTVCAWPKSRKQKLEKQNSLEYMDNDRLKPEADTLPRSG 300
 QY 301 EQERKNPMALYILKDKSPETEENPAPEPRSATPEPGPGYSVSPAVGPRSPGLPIRSARR 360
 DB 301 EQERKNPMALYILKDKSPETEENPAPEPRSATPEPGPGYSVSPAVGPRSPGLPIRSARR 360
 QY 361 YPRSPARSPATGRTHSSPPRAPPSPGSRASRTLRTAGVHIIREQDEAGPVEISA 416
 DB 361 YPRSPARSPATGRTHSSPPRAPPSPGSRASRTLRTAGVHIIREQDEAGPVEISA 416

RESULT 4
 ADS11056
 ID ADS11056 standard; protein; 416 AA.

XX ADS11056;
 AC 16-DEC-2004 (first entry)
 DT
 DE Human therapeutic protein - SEQ ID 1293.
 XX
 KW antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
 KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
 KW aplastic anaemia; cancer; wound healing; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO2004080148-A2.
 XX
 PD 23-SEP-2004.
 XX
 PF 30-SEP-2003; 2003WO-US030720.
 XX
 PR 02-OCT-2002; 2002US-0416186P.
 XX
 PA (NUVE-) NUVELO INC.
 XX
 PI Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
 PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
 XX WPI; 2004-668857/65.
 DR N-PSDB; ADS10372.
 XX
 CC New polynucleotide, useful in preparing a composition for diagnosing or
 CC treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
 CC aplastic anemia or cancer for promoting wound healing.
 XX
 PS Claim 20; SEQ ID NO 1293; 718pp; English.
 XX
 CC The invention relates to a novel isolated polynucleotide and the encoded
 CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
 CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
 CC be useful in preparing a composition for diagnosing or treating
 CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
 CC disorders, such as aplastic anaemia or cancer, as well as for promoting
 CC wound healing. The molecules may also be utilised during gene therapy
 CC procedures. The current sequence is that of a human therapeutic protein
 CC of the invention. The current sequence is not shown explicitly within the
 CC specification but can be accessed from the WIPO web-site.
 XX
 SQ Sequence 416 AA;
 Query Match 100.0%; Score 2122; DB 8; Length 416;
 Best Local Similarity 100.0%; Pred. No. 2.4e-146;
 Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKRERGALSASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTGKSAALLSVQYSST 60
 DB 1 MKRERGALSASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTGKSAALLSVQYSST 60
 QY 61 SSDRPVVKWQLKRDKPVTWQSIGTEVIGTLRPDYDRIRLRFENGSLLLSDQLADEGTY 120
 DB 61 SSDRPVVKWQLKRDKPVTWQSIGTEVIGTLRPDYDRIRLRFENGSLLLSDQLADEGTY 120
 QY 121 EVEISITDDTFTGKTNLTVDVPISRPQVLVASTTTLSEAFTLNCSHENGTKPSYTW 180
 DB 121 EVEISITDDTFTGKTNLTVDVPISRPQVLVASTTTLSEAFTLNCSHENGTKPSYTW 180
 QY 181 LKDGKPLNDSRMLLSPDKQLTITRVLMEDDDLKQNSLEYMDNDRLKPEADTLPRSG 240
 DB 181 LKDGKPLNDSRMLLSPDKQLTITRVLMEDDDLKQNSLEYMDNDRLKPEADTLPRSG 240
 QY 241 LYIILSTGGIFLLVTLTVCAWPKSRKQKLEKQNSLEYMDNDRLKPEADTLPRSG 300
 DB 241 LYIILSTGGIFLLVTLTVCAWPKSRKQKLEKQNSLEYMDNDRLKPEADTLPRSG 300
 QY 301 EQERKNPMALYILKDKSPETEENPAPEPRSATPEPGPGYSVSPAVGPRSPGLPIRSARR 360

CC infections, cancer, inflammation, allergies, graft rejection,
 CC atherosclerosis, hypertension, osteoporosis, anaemia, Alzheimer's
 CC disease, Parkinson's disease, asthma, diabetes, myocardial infarction or
 CC haemophilia). They may also be used as targets in drug screening. The
 CC present sequence represents a polypeptide of the invention.

XX SQ Sequence 383 AA;

Query Match 92.5%; Score 1962; DB 8; Length 383;
 Best Local Similarity 100.0%; Pred. No. 1e-134;
 Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 VNITSPVRLHGTGKSAALLSVQSSSTSDRPVVKQLKRDKPVTVQSIGTEVIGTLRP 93
 Db 1 VNITSPVRLHGTGKSAALLSVQSSSTSDRPVVKQLKRDKPVTVQSIGTEVIGTLRP 60
 Qy 94 DYDRIRLRFENGSLLSLDLQADGTYEVEISITDDTFTGKTNLTVDVPIRPOVLVA 153
 Db 61 DYDRIRLRFENGSLLSLDLQADGTYEVEISITDDTFTGKTNLTVDVPIRPOVLVA 120
 Qy 154 STTVLELSEAFLLNCSEHNGTKPSYTLKDGKPLLLNDSRMLLSPDKVLTITRVLMEDD 213
 Db 121 STTVLELSEAFLLNCSEHNGTKPSYTLKDGKPLLLNDSRMLLSPDKVLTITRVLMEDD 180
 Qy 214 LYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLTVCAKWKPSKRRKQKL 273
 Db 181 LYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLTVCAKWKPSKRRKQKL 240
 Qy 274 EKQNSLEYMDQNDRLKPEADTLPRSGEQRKNPMALYILKDKOSPETEENPAPEPRSAT 333
 Db 241 EKQNSLEYMDQNDRLKPEADTLPRSGEQRKNPMALYILKDKOSPETEENPAPEPRSAT 300
 Qy 334 EPGPGYSVSPAVGSRPLGPIRSGRRYPRSPATGRTHSSPPRAPPSPGSRSSASR 393
 Db 301 EPGPGYSVSPAVGSRPLGPIRSGRRYPRSPATGRTHSSPPRAPPSPGSRSSASR 360
 Qy 394 TLRTAGVHIIREQDEAGPVEISA 416
 Db 361 TLRTAGVHIIREQDEAGPVEISA 383

RESULT 7

ID ADQ65357 standard; protein; 367 AA.

XX AC ADQ65357;

XX DT 07-OCT-2004 (first entry)

XX DE Novel human protein sequence #330.

XX KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
 KW gene therapy; diagnostic marker; morbid state; osteoporosis;
 KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
 KW cancer.

XX OS Homo sapiens.

XX FN EPI440981-A2.

XX PD 28-JUL-2004.

XX PF 21-JAN-2004; 2004EP-00001196.

XX PR 21-JAN-2003; 2003JP-00102206.

XX PR 09-MAY-2003; 2003JP-00131392.

XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX PI Isogai T, Sugiyama T, Otsuki T, Wakanatsu A, Sato H, Ishii S;

XX PI Yamamoto J, Isono Y, Nagai K, Irie R;

XX DR WPI; 2004-535376/52.

DR N-PSDB; ADQ63169.

XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
 PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
 XX Claim 1; SEQ ID NO 2518; 2449pp; English.

CC The invention relates to 2495 novel polynucleotides (I) and their encoded
 CC polypeptides, sequences hybridizing to these nucleotides, sequences
 CC encoding partial polypeptides and sequences having 70% or 90% identity to
 CC the nucleotide and protein sequences. The nucleotides and polypeptides
 CC are useful as diagnostic markers or therapeutic target for the diseases
 CC or morbid states. They are also useful for treating osteoporosis,
 CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
 CC dementia and various cancers. This sequence corresponds to a protein
 CC sequence of the invention.

XX SQ Sequence 367 AA;

Query Match 69.7%; Score 1478.5; DB 8; Length 367;
 Best Local Similarity 84.7%; Pred. No. 1.9e-99;
 Matches 305; Conservative 12; Mismatches 26; Indels 17; Gaps 4;

Qy 1 MKERGALSASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTGKSAALLSVQSSST 60

Db 1 MKERGALSASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTGKSAALLSVQSSST 60

Qy 61 SSORPVVKWQKRDKPVTVQSIGTEVIGTLRDPYDRIRLRFENGSLLSLDLQADGTY 120

Db 61 SSORPVVKWQKRDKPVTVQSIGTEVIGTLRDPYDRIRLRFENGSLLSLDLQADGTY 120

Qy 121 EVESITDDTFTGKTNLTVDVPIRPOVLVASTTVLELSEAFLLNCSEHNGTKPSYTW 180

Db 121 EVESITDDTFTGKTNLTVDVPIRPOVLVASTTVLELSEAFLLNCSEHNGTKPSYTW 180

Qy 181 LKDGKPLNDSRMLLSPDKVLTITRVLMEDDDLVSCMVENPISQGRSLPVKITVYRRSS 240

Db 181 LKDGKPLNDSRMLLSPDKVLTITRVLMEDDDLVSCMVENPISQGRSLPVKITVYRRSS 240

Qy 241 LYIILSTGGIFLLVTLTVCAKWKPSKRRKQKLEKQNSLEYMDQNDRLKPEADTLPRSG 300

Db 241 LYIILSTGGIFLLVTLTVCAKWKPSKRRKQKLEKQNSLEYMDQNDRLKPEGS-LPAT- 298

Qy 301 EQERKNPMALYI-----LKDKOSPETEENPAPEPRSPATEPGPGYSVSPAVPGR 349

Db 299 ----QSPIPSTIRSGCWKXAEIOLDKENSAGTLPDLGASKGKEPEPASLASHSLPRR 354

RESULT 8

ID AAE14784

XX AC AAE14784 standard; protein; 298 AA.

XX AC AAE14784;

XX DT 30-OCT-2002 (first entry)

XX DE Human immunoglobulin superfamily protein (IGSF-4).

XX KW Human; immunoglobulin superfamily protein-4; IGSPF-4; asthma;
 KW immune system disorder; acquired immune deficiency syndrome; AIDS;
 KW atherosclerosis; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; developmental disorder; renal tubular acidosis;
 KW anaemia; muscle disorder; cardiomyopathy; myocarditis; cancer;
 KW cell proliferative disorder; arteriosclerosis; hepatitis.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

XX FT Peptide 1..33

XX FT Protein 34..298

XX FT Region 43..231

XX FT /label= Signal_peptide

XX FT /note= "Mature IGSPF-4"

FT /note= "Antigen precursor signal immunoglobulin fold
FT glycoprotein T cell surface transmembrane"
FT 48..120
FT /label= Immunoglobulin_domain
FT 161..219
FT /label= Immunoglobulin_domain
FT 243..263
FT /label= Transmembrane_domain
XX
FN WO200240671-A2.
XX
XX 23-MAY-2002.
XX
XX 15-NOV-2001; 2001WO-US044974.
XX
XX 16-NOV-2000; 2000US-0249645P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Baughn MR, Lu DAM, Yue H, Elliott VS, Thangavelu K, Ramkumar J;
PI Lu Y, Lo TP, Gururajan R, Gandhi AR, Arvizu C, Yao MG;
XX
XX WPI; 2002-519384/55.
XX N-PSDB; AAD36780.
XX
XX Novel human immunoglobulin superfamily polypeptide, useful in diagnosis,
PT prevention or treatment of immune system, neurological, developmental,
PT muscle and cell proliferative disorders.
XX
XX
XX Claim 1; Page 109-110; 122pp; English.
XX
XX The present sequence is human immunoglobulin superfamily protein (IGSFP) -
CC 4. The IGSFP polypeptide and polynucleotide are useful for diagnosing,
CC treating or preventing disorders associated with aberrant expression of
CC IGSFP e.g. immune system disorders (e.g. acquired immune deficiency
CC syndrome (AIDS), asthma, atherosclerosis, psoriasis, uveitis),
CC neurological disorders (e.g. Alzheimer's disease, Huntington's disease,
CC dementia, Parkinson's disease), developmental disorders (e.g. renal
CC tubular acidosis, epilepsy, anaemia), muscle disorders (e.g.
CC cardiomyopathy, myocarditis), or cell proliferative disorders (e.g.
CC arteriosclerosis, cirrhosis, hepatitis, and cancer). The polypeptide and
CC polynucleotide are also useful for assessing the effects of exogenous
CC compounds on their expression. The polypeptide is useful in drug
CC screening techniques, to analyse the proteome of a tissue or cell type,
CC as elements on a microarray. The polynucleotide is useful for creating
CC knock-in humanised animals or transgenic animals to model human diseases,
CC in somatic or germline gene therapy, to generate a transcript image of a
CC tissue or cell type, for detecting differences in the chromosomal
CC location due to translocation, inversion among normal, carrier or
CC affected individuals, and as hybridisation probes for mapping naturally
CC occurring genomic sequences
XX
SQ Sequence 298 AA;

Query Match 69.4%; Score 1472; DB 5; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.2e-99;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKRGALSRSALRLAPFVYLLLIQTDPLEGNITSPVRLIHGTGKSAALLSVQYSST 60
Db 1 MKRGALSRSALRLAPFVYLLLIQTDPLEGNITSPVRLIHGTGKSAALLSVQYSST 60

Qy 61 SSDRPVVKWQKRPVTVVOSIGTEVIGTIRPDYDRIRLFENGSLLSLQLADSGTY 120
Db 61 SSDRPVVKWQKRPVTVVOSIGTEVIGTIRPDYDRIRLFENGSLLSLQLADSGTY 120

Qy 121 EVEISITDDTFTGKTLNLTVDVPISRPQVLVASTTVLELSAFTLNCSENGTKPSYTW 180
Db 121 EVEISITDDTFTGKTLNLTVDVPISRPQVLVASTTVLELSAFTLNCSENGTKPSYTW 180

Qy 181 LKDGKPLNDSRMLSPQKQVLTTRVLMEDDDLLSCMVENPISQGRSLPVKITVYRRSS 240
Db 181 LKDGKPLNDSRMLSPQKQVLTTRVLMEDDDLLSCMVENPISQGRSLPVKITVYRRSS 240

Qy 241 LYIILSTGGIFLLVTLTVTCACWKPSKRKQKLEKONSLEYMDQNDRLKP 291
Db 241 LYIILSTGGIFLLVTLTVTCACWKPSKRKQKLEKONSLEYMDQNDRLKP 291

RESULT 9
ADO47887
ID ADO47887 standard; protein; 270 AA.
XX
AC ADO47887;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human protein SEQ ID NO:4.
XX
KW human; virucide; anti-HIV; cytostatic; antiinflammatory; anti-allergic;
KW immunosuppressive; antiarteriosclerotic; hypotensive; osteopathic;
KW antianaemic; neuroprotective; nootropic; antiparkinsonian; antiasthmatic;
KW haemostatic; antidiabetic; cardiant; HIV; viral infection; cancer;
KW inflammation; allergy; graft rejection; atherosclerosis; hypertension;
KW osteoporosis; anaemia; Alzheimer's disease; Parkinson's disease; asthma;
KW diabetes; myocardial infarction; haemophilia.
XX
OS Homo sapiens.
XX
PN WO2004007672-A2.
XX
PD 22-JAN-2004.
XX
XX 09-JUL-2003; 2003WO-US021703.
XX
XX 12-JUL-2002; 2002US-0395402P.
XX
PA (NUVE-) NUVELO INC.
XX
PI Rupp F, Wang J, Zhou P, Wehrman T, Wang ZW, Tang YT;
XX WPI; 2004-122914/12.
XX N-PSDB; ADO47886.
XX
XX New isolated polypeptides and polynucleotides useful in diagnostics,
XX forensics, in preventing or treating diseases such as HIV and cancer, and
XX as drug targets.
XX
XX Claim 10; SEQ ID NO 4; 205pp; English.
XX
XX The invention relates to novel isolated polynucleotides and polypeptides
XX encoded by them. Also included are mutants or variants of the
XX polynucleotides and polypeptides. A polypeptide of the invention has
XX virucide, anti-HIV, cytostatic, antiinflammatory, anti-allergic,
XX immunosuppressive, antiarteriosclerotic, hypotensive, osteopathic,
XX antianaemic, neuroprotective, nootropic, antiparkinsonian, antiasthmatic,
XX haemostatic, antidiabetic, and cardiant activity. The composition and
XX methods are useful in diagnostics, forensics, gene or chromosome mapping,
XX identification of mutations responsible for genetic disorders or other
XX traits, in assessing biodiversity, or in producing many other types of
XX data and products dependent on DNA and amino acid sequences. They may
XX also be used in preventing or treating diseases (e.g. HIV and other viral
XX infections, cancer, inflammation, allergies, graft rejection,
XX atherosclerosis, hypertension, osteoporosis, anaemia, Alzheimer's
XX disease, Parkinson's disease, asthma, diabetes, myocardial infarction or
XX haemophilia). They may also be used as targets in drug screening. The
XX present sequence represents a polypeptide of the invention.
XX
SQ Sequence 270 AA;

Query Match 63.7%; Score 1352; DB 8; Length 270;
Best Local Similarity 100.0%; Pred. No. 2.1e-90;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKRGALSRSALRLAPFVYLLLIQTDPLEGNITSPVRLIHGTGKSAALLSVQYSST 60

Db 1 MKRERGALSASRALRLAPFVYLLLIOTDPLEGVNITSPVRLIHGTVKGSALLSVOYSST 60
Qy 61 SSDRPVVKWQKRDKPVTWVQSIGTEVIGTLRPDPYRDRIRLFENGSLILSDLOADEGTY 120
Db 61 SSDRPVVKWQKRDKPVTWVQSIGTEVIGTLRPDPYRDRIRLFENGSLILSDLOADEGTY 120
Qy 121 EVEISITDDTFTGEXTINLTVDVPISRPQVLVASTTVLELSEAFPLNCSEHNGTKPSYTW 180
Db 121 EVEISITDDTFTGEXTINLTVDVPISRPQVLVASTTVLELSEAFPLNCSEHNGTKPSYTW 180
Qy 181 LKDGKPLNDSRMLLSPDQKVLITTRVLMEDDDLYSCWENPISQGRSLPVKITVYRRSS 240
Db 181 LKDGKPLNDSRMLLSPDQKVLITTRVLMEDDDLYSCWENPISQGRSLPVKITVYRRSS 240
Qy 241 LYIILSTGGIFLLVTLVTVCAWKPSKR 268
Db 241 LYIILSTGGIFLLVTLVTVCAWKPSKR 268

RESULT 10

ADSI11055
ID ADSI11055 standard; protein; 270 AA.

XX AC ADSI11055;

DT 16-DEC-2004 (first entry)

XX DE Human therapeutic protein - SEQ ID 1292.

XX KW antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
XX KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
XX KW aplastic anaemia; cancer; wound healing; gene therapy.

XX OS Homo sapiens.

XX PN WO2004080148-A2.

XX PD 23-SEP-2004.

XX PF 30-SEP-2003; 2003WO-US030720.

XX PR 02-OCT-2002; 2002US-0416186P.

XX PA (NUVE-) NUVELO INC.

XX PI Tang YT, Asundi V, Ren P, Zhang J, Zhang J, Wehrman T, Wang Z, Ma Y;
XX PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;

XX DR WPI; 2004-668857/65.

XX DR N-PSDB; ADS10371.

XX PT New polynucleotide, useful in preparing a composition for diagnosing or
XX PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
XX PT aplastic anemia or cancer for promoting wound healing.

XX PS Claim 20; SEQ ID NO 1292; 718pp; English.

XX CC The invention relates to a novel isolated polynucleotide and the encoded
XX CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
XX CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
XX CC be useful in preparing a composition for diagnosing or treating
XX CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
XX CC disorders, such as aplastic anaemia or cancer, as well as for promoting
XX CC wound healing. The molecules may also be utilised during gene therapy
XX CC procedures. The current sequence is that of a human therapeutic protein
XX CC of the invention. The current sequence is not shown explicitly within the
XX CC specification but can be accessed from the WIPO web-site.

XX SQ Sequence 270 AA;

Query Match 63.7%; Score 1352; DB 8; Length 270;
Best Local Similarity 100.0%; Pred. No. 2.1e-90;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKRERGALSASRALRLAPFVYLLLIOTDPLEGVNITSPVRLIHGTVKGSALLSVOYSST 60
Db 1 MKRERGALSASRALRLAPFVYLLLIOTDPLEGVNITSPVRLIHGTVKGSALLSVOYSST 60
Qy 61 SSDRPVVKWQKRDKPVTWVQSIGTEVIGTLRPDPYRDRIRLFENGSLILSDLOADEGTY 120
Db 61 SSDRPVVKWQKRDKPVTWVQSIGTEVIGTLRPDPYRDRIRLFENGSLILSDLOADEGTY 120
Qy 121 EVEISITDDTFTGEXTINLTVDVPISRPQVLVASTTVLELSEAFPLNCSEHNGTKPSYTW 180
Db 121 EVEISITDDTFTGEXTINLTVDVPISRPQVLVASTTVLELSEAFPLNCSEHNGTKPSYTW 180
Qy 181 LKDGKPLNDSRMLLSPDQKVLITTRVLMEDDDLYSCWENPISQGRSLPVKITVYRRSS 240
Db 181 LKDGKPLNDSRMLLSPDQKVLITTRVLMEDDDLYSCWENPISQGRSLPVKITVYRRSS 240
Qy 241 LYIILSTGGIFLLVTLVTVCAWKPSKR 268
Db 241 LYIILSTGGIFLLVTLVTVCAWKPSKR 268

RESULT 11

ABG75380

ID ABG75380 standard; protein; 246 AA.

XX AC ABG75380;

DT 22-APR-2004 (first entry)

XX DE INSP052 extracellular domain protein.

XX KW INSP052; human; cell proliferation; autoimmune disease; inflammation;
XX KW cardiovascular disease; neurological disease; psychiatric disease;
XX KW developmental disease; metabolic disorder; infection;
XX KW immunoglobulin domain-containing cell surface recognition molecule.

XX OS Unidentified.

XX PN WO2003093316-A2.

XX PD 13-NOV-2003.

XX PF 30-APR-2003; 2003WO-GB001851.

XX PR 30-APR-2002; 2002GB-00009884.

XX PA (ARES-) ARES TRADING SA.

XX PI Davids AR, Fagan RJ, Phelps CB, Power C;

XX DR WPI; 2003-903655/82.

XX DR N-PSDB; ACH01279.

XX PT New INSP052 polypeptides and nucleic acids, useful in diagnosing and
XX PT treating cell proliferative, autoimmune/inflammatory, cardiovascular,
XX PT neurological, psychiatric, developmental, genetic or metabolic disorder.

XX PS Claim 1; Fig 7; Opp; English.

XX CC The present invention provides the protein and coding sequences of a
XX CC novel human immunoglobulin domain-containing cell surface recognition
XX CC molecule known as INSP052. The polypeptide is useful as immunoglobulin
XX CC domain-containing cell surface recognition molecule. The sequences may
XX CC also be used in therapy or diagnosing a disease or in the manufacture of
XX CC a medicament for treating a disease. The disease is a cell proliferative,
XX CC autoimmune/inflammatory, cardiovascular, neurological, psychiatric,
XX CC developmental, genetic or metabolic disorder, an infection or other
XX CC pathological condition. The polypeptides and nucleic acids are essential
XX CC to the structural integrity and homeostatic functioning of most tissues.
XX CC The present sequence is a polypeptide shown in the invention

XX SQ Sequence 246 AA;

Query Match 56.8%; Score 1205; DB 7; Length 246;
 Best Local Similarity 100.0%; Pred. No. 1e-79;
 Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRERGALSRRALRLAPFVYLLLIQTDPLEGVNTSPVRLIHGTGKSAALLSVQYSST 60
 DB 1 MKRERGALSRRALRLAPFVYLLLIQTDPLEGVNTSPVRLIHGTGKSAALLSVQYSST 60

QY 61 SSDRPVVKWQKRDKPVTVQSIGTEVIGTIRLPYDRIRLRFENGSLLLSDQLADSGTY 120
 DB 61 SSDRPVVKWQKRDKPVTVQSIGTEVIGTIRLPYDRIRLRFENGSLLLSDQLADSGTY 120

QY 121 EVELSIITDDFTFGKTLNLTVDVPSRPQVLVASTTVLELSEAFNLCSHENGTKPSYTW 180
 DB 121 EVELSIITDDFTFGKTLNLTVDVPSRPQVLVASTTVLELSEAFNLCSHENGTKPSYTW 180

QY 181 LKDGKPLNDSRMLSPDQKVLITTRVLMEDDDLLYSQWENPISQGRSLPVKITVYRRSS 240
 DB 181 LKDGKPLNDSRMLSPDQKVLITTRVLMEDDDLLYSQWENPISQGRSLPVKITVYRRSS 240

RESULT 12
 ADO47890
 ADO47890 standard; protein; 237 AA.

AC ADO47890;
 XX
 XX 15-JUL-2004 (first entry)
 XX
 XX Human mature protein SEQ ID NO:7.
 XX
 XX human; virucide; anti-HIV; cytostatic; antiinflammatory; antiallergic;
 KW immunosuppressive; antiarteriosclerotic; hypotensive; osteopathic;
 KW antianaemic; neuroprotective; nootropic; antiparkinsonian; antiasthmatic;
 KW haemostatic; antidiabetic; cardiant; HIV; viral infection; cancer;
 KW inflammation; allergy; graft rejection; atherosclerosis; hypertension;
 KW osteoporosis; anaemia; Alzheimer's disease; Parkinson's disease; asthma;
 KW diabetes; myocardial infarction; haemophilia.

OS Homo sapiens.

XX WO2004007672-A2.

XX 22-JAN-2004.

XX 09-JUL-2003; 2003WO-US021703.

XX 12-JUL-2002; 2002US-0395402P.

XX (NUVE-) NUVELO INC.

XX Rupp F, Wang J, Zhou P, Wehrman T, Wang ZW, Tang YT;

XX WPI; 2004-122914/12.

XX N-PSDB; ADO47888.

XX New isolated polypeptides and polynucleotides useful in diagnostics,
 PT forensics, in preventing or treating diseases such as HIV and cancer, and
 PT as drug targets.

XX Claim 10; SEQ ID NO 7; 205pp; English.

XX The invention relates to novel isolated polynucleotides and polypeptides
 CC encoded by them. Also included are mutants or variants of the
 CC polynucleotides and polypeptides. A polypeptide of the invention has
 CC virucide, anti-HIV, cytostatic, antiinflammatory, antiallergic,
 CC immunosuppressive, antiarteriosclerotic, hypotensive, osteopathic,
 CC antianaemic, neuroprotective, nootropic, antiparkinsonian, antiasthmatic,
 CC haemostatic, antidiabetic, and cardiant activity. The composition and
 CC methods are useful in diagnostics, forensics, gene or chromosome mapping,
 CC identification of mutations responsible for genetic disorders or other
 CC traits, in assessing biodiversity, or in producing many other types of

CC data and products dependent on DNA and amino acid sequences. They may
 CC also be used in preventing or treating diseases (e.g. HIV and other viral
 CC infections, cancer, inflammation, allergies, graft rejection,
 CC atherosclerosis, hypertension, osteoporosis, anaemia, Alzheimer's
 CC disease, Parkinson's disease, asthma, diabetes, myocardial infarction or
 CC haemophilia). They may also be used as targets in drug screening. The
 CC present sequence represents a polypeptide of the invention.

XX Sequence 237 AA;

Query Match 56.2%; Score 1192; DB 8; Length 237;
 Best Local Similarity 100.0%; Pred. No. 8.5e-79;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 VNITSVRLIHGTGKSAALLSVQYSSTSDRPVVKWQKRDKPVTVQSIGTEVIGTLRP 93
 DB 1 VNITSVRLIHGTGKSAALLSVQYSSTSDRPVVKWQKRDKPVTVQSIGTEVIGTLRP 60

QY 94 DYDRIRLRFENGSLLLSDQLADEGTYEVEISITDDFTFGKTLNLTVDVPISRPQVLVA 153
 DB 61 DYDRIRLRFENGSLLLSDQLADEGTYEVEISITDDFTFGKTLNLTVDVPISRPQVLVA 120

QY 154 STTVLELSEAFNLCSHENGTKPSYTWLKDGPDLNDSRMLSPDQKVLITRVLMEDDDD 213
 DB 121 STTVLELSEAFNLCSHENGTKPSYTWLKDGPDLNDSRMLSPDQKVLITRVLMEDDDD 180

QY 214 LYSQWENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCAWKPSSKR 268
 DB 181 LYSQWENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCAWKPSSKR 235

RESULT 13

ADM87341

ID ADM87341 standard; protein; 256 AA.

XX ADM87341;

XX 03-JUN-2004 (first entry)

XX Human protein SEQ ID NO:434.

XX respiratory; cytostatic; antiarthritic; antiinflammatory;
 KW gastrointestinal; antibacterial; immunosuppressive; antidiabetic;
 KW antirheumatic; gene therapy; molecular weight marker; chromosome marker;
 KW chromosome tag; genetic fingerprinting; nutritional supplement; cancer;
 KW inflammatory condition; arthritis; inflammatory bowel disease;
 KW Crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1;
 KW graft versus host disease; human.

XX Homo sapiens.

XX WO2004009834-A2.

XX 29-JAN-2004.

XX 19-JUL-2002; 2002WO-US022858.

XX 21-JUL-2001; 2001US-0306971P.

XX 28-MAR-2002; 2002US-00112944.

XX (NUVE-) NUVELO INC.

XX Tang YT, Yang Y, Weng G, Zhang J, Ren F, Xue A, Wang J;

XX Wehrman T, Ghosh MJ, Wang D, Zhao QA, Wang Z;

XX WPI; 2004-143291/14.

XX N-PSDB; ADM87097.

XX New isolated polynucleotides and polypeptides, useful for treating, e.g.
 PT cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease,
 PT Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
 PT versus host disease.

XX

Claim 20; SEQ ID NO 434; 591pp; English.

The present invention describes an isolated polynucleotide (I): (a) comprising a nucleotide sequence selected from SEQ ID NO:1-244; or (b) which encodes a polypeptide with biological activity, where the polynucleotide hybridizes to (I) under stringent hybridisation conditions or has greater than 99% sequence identity with (I). (I) has respiratory, cytosolic, antithrombotic, anti-inflammatory, gastrointestinal, antibacterial, immunosuppressive, antidiabetic and antirheumatic activities, and can be used in gene therapy. (I) can be used for generating polynucleotides encoding chimeric or fusion proteins and heterologous protein sequences. The polynucleotides can be used to express recombinant protein for analysis, characterisation or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridise and discover genes, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to subtract-out known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a gene chip or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunisation techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. The polynucleotides and polypeptides can also be used as nutritional sources or supplements, e.g. as a protein or amino acid supplement, as a carbon source, as a nitrogen source or as a source of carbohydrates. The polynucleotides and polypeptides can also be used to treat cancer. The compositions are useful for promoting better or faster closure of non-healing wounds, for the generation and regeneration of tissues, for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage. The compositions can also be used to treat inflammatory conditions (e.g. arthritis, inflammatory bowel disease or Crohn's disease), sepsis, rheumatoid arthritis, diabetes mellitus type 1 or graft versus host disease. The present sequence represents a novel human polypeptide sequence from the present invention. N.B. The sequences for this patent were obtained from the USPTO web site from an equivalent US patent US20040048249A1.

Sequence 256 AA;

Query Match 56.0%; Score 1189; DB 8; Length 256;
Best Local Similarity 96.7%; Pred. No. 1.6e-78;
Matches 236; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

```
Qy 1 MKRERGALSRSARLRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTGKSALLSVQYSST 60
Db 1 MKRERGALSRSARLRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTGKSALLSVQYSST 60

Qy 61 SSDRPVVKWQKRDKPVTWQSIGTEVIGTLRDPYDRIRLRFENGSLLSDLQADEGTY 120
Db 61 SSDRPVVKWQKRDKPVTWQSIGTEVIGTLRDPYDRIRLRFENGSLLSDLQADEGTY 120

Qy 121 EVEISITDDTFTGKTLINLTVDVPIRPPQVLVASTTTLVLESEATFLNCSHENGKPSYTW 180
Db 121 EVEISITDDTFTGKTLINLTVDVPIRPPQVLVASTTTLVLESEATFLNCSHENGKPSYTW 180

Qy 181 LKDGKPLNDSRMLLSPDKQKVLITRVLMEDDDDLYSCWVENPISQGRSLPKVITVYRRSS 240
Db 181 LKDGKPLNDSRMLLSPDKQKVLITRVLMEDDDDLYSCWVENPISQGRSLPKVITVYRRSS 240

Qy 241 LYII 244
Db 241 FYII 244
```

RESULT 14

AAM24238

ID AAM24238 standard; protein; 256 AA.

XX

AC AAM24238;

12-OCT-2001 (first entry)

Human EST encoded protein SEQ ID NO: 1763.

Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
gene therapy; nutrition.

Homo sapiens.

WO200154477-A2.

02-AUG-2001.

25-JAN-2001; 2001WO-US002687.

25-JAN-2000; 2000US-00491404.

17-JUL-2000; 2000US-00617746.

03-AUG-2000; 2000US-00631451.

15-SEP-2000; 2000US-00663870.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

Cao Y, Drmanac RA, Zhang J, Werhman T;

WPI; 2001-476164/51.

N-PSDB; AAH98897.

Isolated polypeptide for treatment of diseases, diagnostics, raising
antibodies and research use.

Claim 20; Page 1159-1160; 1275pp; English.

The present invention provides the protein and coding sequences of novel
proteins from a variety of organisms, including human, dog, cat, horse,
cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
urchin and tomato. These were derived from expressed sequence tags (ESTs)
from the organism of interest. They can be used in diagnostics,
forensics, gene mapping, identification of mutations, to assess
biodiversity and for nutritional purposes. The present sequence is a
protein of the invention

Sequence 256 AA;

Query Match 55.5%; Score 1178; DB 4; Length 256;
Best Local Similarity 97.1%; Pred. No. 9.9e-78;
Matches 234; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

```
Qy 1 MKRERGALSRSARLRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTGKSALLSVQYSST 60
Db 1 MKRERGALSRSARLRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTGKSALLSVQYSST 60

Qy 61 SSDRPVVKWQKRDKPVTWQSIGTEVIGTLRDPYDRIRLRFENGSLLSDLQADEGTY 120
Db 61 SSDRPVVKWQKRDKPVTWQSIGTEVIGTLRDPYDRIRLRFENGSLLSDLQADEGTY 120

Qy 121 EVEISITDDTFTGKTLINLTVDVPIRPPQVLVASTTTLVLESEATFLNCSHENGKPSYTW 180
Db 121 EVEISITDDTFTGKTLINLTVDVPIRPPQVLVASTTTLVLESEATFLNCSHENGKPSYTW 180

Qy 181 LKDGKPLNDSRMLLSPDKQKVLITRVLMEDDDDLYSCWVENPISQGRSLPKVITVYRRSS 240
Db 181 LKDGKPLNDSRMLLSPDKQKVLITRVLMEDDDDLYSCWVENPISQGRSLPKVITVYRRSS 240

Qy 241 L 241
Db 241 L 241
```

RESULT 15

ADM87787
ID ADM87787 standard; protein; 256 AA.
XX
AC ADM87787;
XX
XX 03-JUN-2004 (first entry)
XX
XX Human EST derived amino acid sequence SEQ ID NO:880.
XX
XX respiratory; cytostatic; antiarthritic; antiinflammatory;
KW gastrointestinal; antibacterial; immunosuppressive; antidiabetic;
KW antirheumatic; gene therapy; molecular weight marker; chromosome marker;
KW chromosome tag; genetic fingerprinting; nutritional supplement; cancer;
KW inflammatory condition; arthritis; inflammatory bowel disease;
KW Crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1;
KW graft versus host disease; human; expressed sequence tag; EST.
XX
XX Homo sapiens.
XX
XX WO2004009834-A2.
XX
XX 29-JAN-2004.
XX
XX 19-JUL-2002; 2002WO-US022858.
XX
XX 21-JUL-2001; 2001US-0306971P.
XX
XX 28-MAR-2002; 2002US-00112944.
XX
XX (NUVE-) NUVELO INC.
XX
XX Tang YT, Yang Y, Weng G, Zhang J, Ren F, Xue A, Wang J;
PI Wehrman T, Ghosh MJ, Wang D, Zhao QA, Wang Z;
XX
XX WPI; 2004-143291/14.
XX
XX N-PSDB; ADM87569.
XX
XX New isolated polynucleotides and polypeptides, useful for treating, e.g.
PT cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease,
PT Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
PT versus host disease.
XX
XX Example 2; SEQ ID NO 880; 591pp; English.
XX
XX The present invention describes an isolated polynucleotide (I): (a)
XX comprising a nucleotide sequence selected from SEQ ID NO:1-244; or (b)
XX which encodes a polypeptide with biological activity, where the
XX polynucleotide hybridises to (I) under stringent hybridisation conditions
XX or has greater than 99% sequence identity with (I). (I) has respiratory,
XX cytostatic, antiarthritic, antiinflammatory, gastrointestinal,
XX antibacterial, immunosuppressive, antidiabetic and antirheumatic
XX activities, and can be used in gene therapy. (I) can be used for
XX generating polynucleotides encoding chimeric or fusion proteins and
XX heterologous protein sequences. The polynucleotides can be used to
XX express recombinant protein for analysis, characterisation or therapeutic
XX use; as markers for tissues in which the corresponding protein is
XX preferentially expressed; as molecular weight markers on gels; as
XX chromosome markers or tags to identify chromosomes or to map related gene
XX positions; to compare with endogenous DNA sequences in patients to
XX identify potential genetic disorders; as probes to hybridise and discover
XX genes, related DNA sequences; as a source of information to derive PCR
XX primers for genetic fingerprinting; as a probe to subtract-out known
XX sequences in the process of discovering other novel polynucleotides; for
XX selecting and making oligomers for attachment to a gene chip or other
XX support, including for examination of expression patterns; to raise anti-
XX protein antibodies using DNA immunisation techniques; and as an antigen
XX to raise anti-DNA antibodies or elicit another immune response. The
XX polynucleotides and polypeptides can also be used as nutritional sources
XX or supplements, e.g. as a protein or amino acid supplement, as a carbon
XX source, as a nitrogen source or as a source of carbohydrates. The
XX polynucleotides and polypeptides can also be used to treat cancer. The
XX compositions are useful for promoting better or faster closure of non-
XX healing wounds, for the generation and regeneration of tissues, for gut
XX protection or regeneration and treatment of lung or liver fibrosis,

CC reperfusion injury in various tissues, and conditions resulting from
CC systemic cytokine damage. The compositions can also be used to treat
CC inflammatory conditions (e.g. arthritis, inflammatory bowel disease or
CC Crohn's disease), sepsis, rheumatoid arthritis, diabetes mellitus type 1
CC or graft versus host disease. The present sequence represents an
CC expressed sequence tag (EST) derived amino acid sequence from the present
CC invention. N.B. The sequences for this patent were obtained from the
CC USPTO web site from an equivalent US patent US20040048249A1.
XX
XX Sequence 256 AA;
Query Match 55.5%; Score 1178; DB 8; Length 256;
Best Local Similarity 97.1%; Pred. No. 9.9e-78;
Matches 234; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 MKERGALSASRALRLAPFVYLLLTQDPLEGVNITSPVRLIHGTGKSALLSVQYSST 60
DB 1 MKERGALSASRALRLAPFVYLLLTQDPLEGVNITSPVRLIHGTGKSALLSVQYSST 60
QY 61 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYDRDLRFLFENGSLLLSDQLADEGTY 120
DB 61 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYDRDLRFLFENGSLLLSDQLADEGTY 120
QY 121 EVEISITDDTFTGCKTINLTVDVPISRPQVLGASTTVLSEAFITLNCSENGTKPSYTW 180
DB 121 EVEISITDDTFTGCKTINLTVDVPISRPQVLGASTTVLSEAFITLNCSENGTKPSYTW 180
QY 181 LKDGKPLNDSRMLLSPDQKVLITRVLMEDDDLVSCWVENPISQGRSLPVKITVVRSS 240
DB 181 LKDGKPLNDSRMLLSPDQKVLITRVLMEDDDLVSCWVENPISQGRSLPVKITVVRSS 240
QY 241 L 241
DB 241 L 241

Search completed: July 26, 2005, 16:07:32
Job time : 120.106 secs

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OM protein - protein search, using sw model

Run on: July 26, 2005, 15:58:02 ; Search time 24.0385 seconds
(without alignments)
1665.085 Million cell updates/sec

Title: US-10-706-691-16
Perfect score: 2122
Sequence: 1 MKRERGALSRSARLRLAPF.....TAGVHIIREQDEAGPVEISA 416

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	220	10.4	351	1 RWHUC2	T-cell surface gly
2	216	10.2	341	2 JC1512	biliary glycoprote
3	207.5	9.8	278	2 JC1506	biliary glycoprote
4	202.5	9.5	278	2 A39037	carcinoembryonic a
5	197.5	9.3	365	2 J37780	coxsackie- and ade
6	194.5	9.2	483	2 T17346	hypothetical prote
7	189	8.9	272	2 I48268	biliary glycoprote
8	188.5	8.9	1091	2 A58532	glial cell membran
9	188	8.9	341	2 JC1511	biliary glycoprote
10	186.5	8.8	458	2 JC1509	biliary glycoprote
11	183.5	8.6	629	2 A46500	ly-9.2 antigen - m
12	181.5	8.6	521	2 S34338	biliary glycoprote
13	180.5	8.5	347	2 S41638	T-cell surface gly
14	179.5	8.5	278	2 JC1507	biliary glycoprote
15	178.5	8.4	475	2 A54879	pregnancy-specific
16	173.5	8.2	344	1 RWRTC2	T-cell surface gly
17	173.5	8.2	853	1 IJUBNC	neural cell adhesi
18	173	8.2	299	2 S56749	junctional adhesio
19	172.5	8.1	858	1 IJRTNC	neural cell adhesi
20	170.5	8.0	526	1 A32164	biliary glycoprote
21	170.5	8.0	1227	2 T23004	hypothetical prote
22	168.5	7.9	475	2 I76668	pregnancy-specific
23	168	7.9	761	1 IJHUNG	neural cell adhesi
24	166	7.8	458	2 S68177	C-CAM2a protein is
25	166	7.8	458	2 S23969	cell-adhesion mole
26	166	7.8	519	2 A44783	ecto-ATPase precu
27	166	7.8	1091	1 IJCHNL	neural cell adhesi
28	164	7.7	464	2 C30127	transmembrane carc
29	163.5	7.7	725	2 J20100	neural cell adhesi

RESULT 1 -
RWHUC2

T-cell surface glycoprotein CD2 precursor - human

N:Alternate names: E rosette receptor; erythrocyte receptor; erythrocyte-binding protein

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1989 #sequence revision 31-Mar-1989 #text change 09-Jul-2004

C:Accession: A28967; A26486; B26486; A28416; A28023; S02232; A30430; S00829; A29874

R:Diamond, D.J.; Clayton, L.K.; Sayre, P.H.; Reinherz, E.L.

Proc. Natl. Acad. Sci. U.S.A. 85, 1615-1619, 1988

A:Title: Exon-intron organization and sequence comparison of human and murine T11 (CD2)

A:Reference number: A28967; MUID:88144486; PMID:2894031

A:Accession: A28967

A:Molecule type: DNA

A:Residues: 1-351 <DIA>

A:Cross-references: UNIPROT:P06729; GB:M19806; GB:J03622; GB:J03623; NID:g180079; PIDN:A

R:Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.

Proc. Natl. Acad. Sci. U.S.A. 83, 8718-8722, 1986

A:Title: Molecular cloning of the human T-lymphocyte surface CD2 (T11) antigen.

A:Reference number: A26486; MUID:87041523; PMID:3490670

A:Accession: A26486

A:Molecule type: mRNA

A:Residues: 1-338,'M',340,'Q'QKTHCPLPLIKKDRNCLFQ' <SE1>

A:Accession: B26486

A:Molecule type: protein

A:Residues: 25-46,'X',50 <SE2>

R:Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.

Proc. Natl. Acad. Sci. U.S.A. 84, 7256, 1987

A:Reference number: A28416

A:Contents: revision

A:Accession: A28416

A:Molecule type: mRNA

A:Residues: 333-351 <SE3>

R:Seed, B.; Aruffo, A.

Proc. Natl. Acad. Sci. U.S.A. 84, 3365-3369, 1987

A:Title: Molecular cloning of the CD2 antigen, the T-cell erythrocyte receptor, by a rap

A:Reference number: A28023; MUID:87204137; PMID:2437578

A:Accession: A28023

A:Molecule type: mRNA

A:Residues: 1-265,'Q',267-351 <SEE>

A:Cross-references: GB:M16445; NID:g178668; PIDN:AAA51738.1; PID:g178669

R:Savre, P.H.; Chang, H.C.; Hussey, R.E.; Brown, N.R.; Richardson, N.E.; Spagnoli, G.; C

Proc. Natl. Acad. Sci. U.S.A. 84, 2941-2945, 1987

A:Title: Molecular cloning and expression of T11 cDNAs reveal a receptor-like structure

A:Reference number: S02292; MUID:87204243; PMID:2883656

A:Accession: S02292

A:Molecule type: mRNA

A:Residues: 1-338,'M',340,'Q'QKTHCPLPLIKKDRNCLFQ' <SA1>

A:Cross-references: GB:M16336; NID:g180093; PIDN:AAA51946.1; PID:g180094

A:Accession: A30430

A:Molecule type: protein

A:Residues: 25-43,152-163 <SA2>

R:Lang, G.; Wotton, D.; Owen, M.J.; Sewell, W.A.; Brown, M.H.; Mason, D.Y.; Crumpton, M.

C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal homology <CEAN>
C:Keywords: glycoprotein; receptor
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F:159-216/Domain: immunoglobulin homology <IMW>
E:87,104,153,195/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.2%; Score 216; DB 2; Length 341;
Best Local Similarity 26.1%; Pred. No. 3.4e-06;
Matches 73; Conservative 48; Mismatches 125; Indels 34; Gaps 9;

Qy	73	RDKPVTVVQSIGTEVIGTLR----	PDYDRIRLFPENGSLLLSDQLADSGTYVEVISITD	128
Dd	69	KGNPVSTNAEIVHQVTGNTTKTTPAHSGRETVYNGSLLIQRTVKDTGVYTIE--MTD	126	
Qy	129	DTF-TGEKTIINLTVDPISRPOVLVASITVLELSAFTLNCSHENGTKPSYTWLKDGKPL	187	
Dd	127	ENFRTEATVFHVHPQTQPGLQVTNITVKEL-DSVTILTCI-SNDIGANIQWLFNQSOL	184	
Qy	188	LNDGRMLSPQKVLTITRVLMEDDDLYSCMVENIPISQGRSLPVKITVYRRSSLYII---	244	
Dd	185	QLTERMTLSQNNSILRIDPIKEADAGEYQCEISNPVSVKRSNSIKLDI-----IFDPT	237	
Qy	245	--LSTG-----GIFLLVTLVTVCWKPSKKQKLEKONSLEYMQNDRLKPEAD	294	
Dd	238	QGGSUDGAIAIGIVGVAGVALIAGLATFLYSRKGGSGDQRDLTEHKFSTSNNLAPSD	297	
Qy	295	TLPRSGEOKRNPMALYILKDQSPETEEPAPEPRSAT E 334		
Dd	298	NSP-----NKVDDVAVYTVLNFNSQQPNRPTSAPSSPRATE 332		

RESULT 3

JC1506
biliary glycoprotein B - mouse
C:Species: Mus musculus (house mouse)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C:Accession: JC1506
R:McCuagig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
A>Title: Expression of the Bgp gene and characterization of mouse colon biliary glycoprotein
A:Reference number: JC1505; MUID:93273228; PMID:8500759
A:Accession: JC1506
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-278 <MCC>
A:Cross-references: UNIPROT:O99232
C:Comment: This protein is expressed at the cell surface and plays a determinant role in
C:Genetics:
A:Gene: Bgpb
C:Superfamily: biliary glycoprotein; carcinoembryonic antigen precursor amino-terminal h
C:Keywords: glycoprotein; receptor
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F:159-216/Domain: immunoglobulin homology <IMW>
E:87,104,153,195/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.8%; Score 207.5; DB 2; Length 278;
Best Local Similarity 32.1%; Pred. No. 8.8e-06;
Matches 54; Conservative 32; Mismatches 73; Indels 9; Gaps 5;

Qy	73	RDKPVTVVQSIGTEVIGTLR----	PDYDRIRLFPENGSLLLSDQLADSGTYVEVISITD	128
Dd	69	KGNPVSTNAEIVHQVTGNTTKTTPAHSGRETVYNGSLLIQRTVKDTGVYTIE--MTD	126	
Qy	129	DTF-TGEKTIINLTVDPISRPOVLVASITVLELSAFTLNCSHENGTKPSYTWLKDGKPL	187	
Dd	127	ENFRTEATVFHVHPQTQPGLQVTNITVKEL-DSVTILTCI-SNDIGANIQWLFNQSOL	184	
Qy	188	LNDGRMLSPQKVLTITRVLMEDDDLYSCMVENIPISQGRSLPVKITV 235		
Dd	185	QLTERMTLSQNNSILRIDPIKEADAGEYQCEISNPVSVKRSNSIKLDI 232		

RESULT 4

Db 127 G- -VGNKKIQTLVLPKPSGIRCYVDGSE--BIGNDFKLKCEPKEGSLPLRYEQK----- 177
 Qy 188 LNDSRML-----LSPDQKVLITITRLMEDDDLYSCWVENPISQGRSLPVKITVYRRS 239
 Db 178 LSDSQKLPKSWLPMTSP---VLSVKNASAEYSGTCTVNRVSGDQCL-LALDVPVPS 233
 Qy 240 S-----LYIILSTGGIFLLVTLVTVCACWPKSPKQKLEKQNSLEYMDQNDRLKPEAD 294
 Db 234 NRACTAGAVIGTLLALVLIALIVFC-CHK--RRBEKYEKE-----VHDIR----- 278
 Qy 295 TLPKSGQERKNPMALYILKDKSPETEENPAPEPRSAPE--GPPGYSVSPAVGRSP 351
 Db 279 -----EDVPPPKSRSTARSYIGSNHSLGMSPSNME 311
 Qy 352 G-----LPFIRSARRYPRSPARSPATGRTHSSPPRAPSPGSR 389
 Db 312 GYSKTQYNQPSSEDLERAPQSP-----TLPPAKVAAPNLSR 347

 RESULT 6
 T17346
 hypothetical protein DKFPz58601624.1 - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T17346
 R:Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, September 1999
 A:Reference number: Z18727
 A:Accession: T17346
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-483 <DUE>
 A:Cross-references: UNIPROT:Q9UF14; EMBL:AL117666
 A:Experimental source: adult uterus; Clone DKFPz58601624
 C:Genetics:
 A:Note: DKFPz58601624.1

 Query Match 9.2%; Score 194.5; DB 2; Length 483;
 Best Local Similarity 21.5%; Pred. No. 0.00011;
 Matches 83; Conservative 55; Mismatches 155; Indels 93; Gaps 13;

 Qy 55 VQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGILRPDYRIRLP---ENGSLLLSD 111
 Db 8 LCAATGCHPNPQIAWQ--KDG-----GTDFPAARER-RMHVMPDDDDVFFITD 51
 Qy 112 LQLADSGTYEVEISITDDFTGKTLNLDVDPISRPQVLVASTTVLLELSEAFLLNC SHE 171
 Db 52 VKIDDAAGV-----SCTAQNSAGSISANALTULETSLVPLBDRVSVSGETVALQCKAT 107
 Qy 172 NGTKPSVYTLKDGKPLNDSRMLLSPDQKVLITITRLMEDDDLYSCWVENPISQGRSLPV 231
 Db 108 GNPPRITWFKGDRPLSLTERHLLTPDNQLLVQNVVAEDAGRYTCMSNTLGTERRA--- 164
 Qy 232 KITVYRRSLIYIILSTG-----GIF-----LLVTLVTVCACWPKSPKQKLEK 275
 Db 165 -----HSQLSVLPAAGCKRGDTGVGIFTIAVSSIVLTSLVWVCIIYQTRKKSE----- 213
 Qy 276 QNSLEYMDQNDRLKPEADTLPRSGQERKNPMALYILKDKSPETE---ENPAPPRSA 332
 Db 214 ----EYSVTNTDFTVVPVDPVPSYLSQGTLSRQETVVRTEGGPQANGHIESNGVCPRDA 269
 Qy 333 TE-PGPPGYSVSPAVGRSPGL-----PIRSARR----- 360
 Db 270 SHFPEDTHISVACRQPLCAGSNHYKPKWAMEKABGTGPHKMEHGRVVCSDCNTEYD 329
 Qy 361 -YPRSPARSPATGRTHSSPPRAPSSP 385
 Db 330 CYSEGGQAFHPQPVSRDQAQPSAPNGP 355

 RESULT 7
 I48268
 biliary glycoprotein - mouse

C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: J48268
R;Nedellec, P.; Dvekel, G.S.; Daniels, E.; Turbide, C.; Chow, B.; Basile, A.A.; Holmes J. Virol. 68, 4525-4537, 1994
A;Title: Bgp2, a new member of the carcinoembryonic antigen-related gene family, encoded A;Reference number: A53995; MUID:94267915; PMID:8207827
A;Accession: J48268
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-272 <RES>
A;Cross-references: UNIPROT:Q8R1N5; EMBL:X76085; NID:9511020; PIDN:CAA53699.1; PID:9511020
C;Genetics:
A;Gene: Bgp2
C;Superfamily: biliary glycoprotein; carcinoembryonic antigen precursor amino-terminal homology <CEAN>
C;Keywords: Glycoprotein
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;159-216/Domain: immunoglobulin homology <IMM>

Query Match 8.9%; Score 189; DB 2; Length 272;
Best Local Similarity 25.4%; Pred. No. 0.00012; Mismatches 100; Indels 48; Gaps 9;
Matches 66; Conservative 46;

Qy 24 LLIQTDPLEGVNITSPVRLIHGTGKSAISV-----QYSSSTSSDRPVVKWQ 70
Db 24 LLASWSPTTAQVTVMAFPLHAAGNNVILVYNNMKGVSFAFSWHKSGTSTNAEIVRFV 83

Qy 71 LKRDKPVTVQSGIGTEVIGTLRPDYRDRIRLFPENGSLLLDLQLADEGTVEVEISITDDT 130
Db 84 TGTNKTIK-----GPVHSGRETLYNSGLLIQRVTMKTGVTYIE--MTDQN 128

Qy 131 F-----TGEKTNLTVDVPISRPQVLASTVLESEAPTLNCSHENGTKPSYTWLKGK 185
Db 129 YRRRVLTGQ-----FHVHKPVTPQSLQVNTNITVKEL-DSVLTCLSKD-RQAHIHWIFNND 182

Qy 186 PLNDSRMLLSPDKQVITITVLMMEDDDLYSCWVENPISQGRSLPVKITVYRRSSLYI-- 243
Db 183 TLLITERMTTSQAGLILKIDPIKEDAGEYQCEISNPVSKRSNIKLEIVFDSTYDISD 242

Qy 244 -----ILSTG-----GIFLLVTL 256
Db 243 VPVIAVITGAVAGVILIAGL 262

RESULT 8
A58532
glial cell membrane glycoprotein LG-1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C;Accession: A58532
R;Suzuki, Y.; Sato, N.; Tohyama, M.; Wanaka, A.; Takagi, T.
J. Biol. Chem. 271, 22522-22527, 1996
A;Title: cDNA cloning of a novel membrane glycoprotein that is expressed specifically in A;Reference number: A58532; MUID:96394313; PMID:8798419
A;Accession: A58532
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1091 <SUZ>
A;Cross-references: UNIPROT:P70193; GB:D78572; NID:g1545806; PIDN:BAAL1416.1; PID:g1545806
F;36-61/Domain: proteoglycan amino-terminal homology <PAH>
F;71-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;95-117/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;118-141/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;142-165/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;166-189/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;191-213/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;214-237/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;238-261/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;262-285/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;286-309/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
F;310-333/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
F;334-357/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
F;358-381/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>

F;385-408/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
F;409-432/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
F;440-485/Domain: proteoglycan carboxyl-terminal homology <PCH>

Query Match 8.9%; Score 188.5; DB 2; Length 1091;
Best Local Similarity 21.1%; Pred. No. 0.00073;
Matches 79; Conservative 56; Mismatches 122; Indels 117; Gaps 16;

Qy 45 GTVGKSAISLVQYSSSTSSDRPVVKWQLKRDKPVTTVQSGIGTEVIGTLRPDYRDRIRLF-- 102
Db 615 GTTAR-----LECAATGHNPNQIAWQ--KDG-----GTDFFPAARER-RHVMV 653

Qy 103 -ENGSLLLDLQLADEGTVEVEISITDDTFTGKTNLTVDVPISRPQVLV-ASTTVLEL 160
Db 654 PDDVFFITDVKIDDMGVY-----SCTAQSAGSVSANILTV-LETPSLAVPLEDRVTV 708

Qy 161 SEAFTLNCSHENGTKPSYTWLKGKPLNDSRMLLSPDKQVLTITRVLMEDDDLYSQWVE 220
Db 709 GETVAFQCKATGSPTPRITWLKGRPLSLTERHHFTFGNQLLVQNNMIDDAGRYTCMS 768

Qy 221 NPISQGRSLPVKITVYRRSLSYILSTG-----GIF-----LLVTLVTVACWK 264
Db 769 NPLGTERA-----HSQSLPILTPGCKKDGTTGIFTIAVVCISLVLSLVVWVLIYQ 819

Qy 265 PSKRKQK-----KLEKQNSLE-----YMDQN----- 285
Db 820 TRKSEYSVNTDEITVPPDVPVSYLSSQGTLSDRQETVVRTEGHOANGHIESNGVCLR 879

Qy 286 DRLKPEADTLPRSGQER-----KNPMALYILKDKD-----SPETE 322
Db 880 DPSLFEVDIHSITCTCRQPKLCVGTREPMKVTREKADRTAAPTHTAHSGVAVCSDCSDTDA 939

Qy 323 ENPAPERSATEPG 336
Db 940 YHPQVPVRDSGQPG 953

RESULT 9

JC1511

biliary glycoprotein G - mouse

C;Species: Mus musculus (house mouse)

C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004

C;Accession: JC1511

R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.

Gene 127, 173-183, 1993

A;Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopro

A;Reference number: JC1505; MUID:93273228; PMID:8500759

A;Accession: JC1511

A;Molecule type: DNA

A;Residues: 1-341 <MCC>

A;Cross-references: UNIPROT:Q61353; GB:X67282

C;Genetics:

A;Gene: Bgpg

C;Superfamily: carcinoembryonic antigen; carcinoembryonic precursor amino-termin

C;Keywords: Glycoprotein; receptor

F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>

F;75-124/Domain: immunoglobulin homology <IMM2>

F;159-216/Domain: immunoglobulin homology <IMM2>

F;71,89,104,153,195/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.9%; Score 188; DB 2; Length 341;

Best Local Similarity 25.2%; Pred. No. 0.00018;

Matches 64; Conservative 45; Mismatches 115; Indels 30; Gaps 8;

Qy 95 YRDRIRLFENGSLLLDLQLADEGTVEVEISITDDTFT-TGEKTNLTVDVPISRPQVLVA 153

Db 95 YSGREIIVSYNSGLLFQMITKMDMGVYTLD--MTDENYRRTQATVRFVHQVPTQFLQVT 152

Qy 154 STTVLELSEAFTLNCSENGTKPSYTWLKGKPLNDSRMLLSPDKQVLTITRVLMEDDD 213

Db 153 NTTVKEL-DSVTLTCL-SNDIGANIOMLFNSQSLQLTERMTLSQNSILRDPKREDAG 210

Qy 214 LYSCHVENPISQGRSLPVKITYRRSSLYII-----LSTG-----GIFLLVTLVTC 260
Db 211 EYQCEISNPVSVRRSNSIKLDI-----IDPTOGGLSDGAIAGIVGVAGVALIAGL 263
Qy 261 ACWPKSRKKQKLLKQNSLEYWDQNDRLKPEADTLPRSGQERKNPMALYILKDKOSPE 320
Db 264 AYFLYSRKSGGSDQDLTEHKPSTNHNLPSONSP-----NKVDDVAYTVLNFNSQOP 318
Qy 321 TEENPAPEPRATE 334
Db 319 NRPTSAPSSPRATE 332

RESULT 10
JC1509
Biliary glycoprotein E - mouse
C:Species: Mus musculus (house mouse)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C:Accession: JC1509
R:McCuag, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
A>Title: Expression of the Bgp gene and characterization of mouse colon biliary glycoprotein
A:Reference number: JC1505; MUID:93273228; PMID:8500759
A:Molecule type: mRNA
A:Genetics: JC1509
A:Residues: 1-458 <MCC>
A:Cross-references: UNIPROT:Q61351; GB:X67280
C:Comment: This protein is expressed at the cell surface and plays a determinant role in
C:Genetics:
A:Gene: Bgpe
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C:Keywords: glycoprotein; receptor
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F:160-219/Domain: immunoglobulin homology <IMM1>
F:254-303/Domain: immunoglobulin homology <IMM2>
F:339-396/Domain: immunoglobulin homology <IMM3>
F:87,104,148,199,206,210,226,258,290,304,333,375/Binding site: carbohydrate (Asn) (C

Query Match 8.8%; Score 186.5; DB 2; Length 458;
Best Local Similarity 27.4%; Pred. No. 0.00032;
Matches 52; Conservative 38; Mismatches 83; Indels 17; Gaps 6;
Qy 73 RDKPVTQVQSIGTEVIGTLR----PDYRDRIRLFENGSLLSLDLQADGTYEVEISITD 128
Db 69 KGNPVTNAEIVHQVTGNTKTTGPAISGRFTVYNSGSLLRVTQVTKDTGYTIE--MTD 126
Qy 129 DTP-TGERTINLTVDVPISRPQVLVASTTVLELSEAFLLNC-SHENGTKPSYTWLKDGP 186
Db 127 ENFRTEATQGFVHPLLLKPNITSNNSPVEGGDSVSLTCDSTDPDNTYLSNRNGES 186
Qy 187 LLNDSRMLSPDQKVLITRVLMEDDDLVSCWENPISQGRSLPVKITYRRSSLY----- 242
Db 187 LSEGDRLKLSGKNTLLNTRNDTGPYCTETRNVPVNSRDPFSLNI-----IYGPDT 241
Qy 243 IILSTGGIFL 252
Db 242 PIISPSDIYL 251

RESULT 11
A46500
Ly-9.2 antigen - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A46500
R:Sandrin, M.S.; Gumley, T.P.; Henning, M.M.; Vaughan, H.A.; Gonsz, L.J.; Trabani, J.A.;
J. Immunol. 149, 1636-1641, 1992
A>Title: Isolation and characterization of cDNA clones for mouse Ly-9.
A:Reference number: A46500; MUID:92373005; PMID:1506686
A:Accession: A46500
A>Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-629 <SAN>

A:Cross-references: GB:M84412; NID:g198931; PIDN:AAA39468.1; PID:g198932
A:Experimental source: C57BL/6
A>Note: sequence extracted from NCBI backbone (NCBIN:111651, NCBIP:111654)
C:Keywords: transmembrane protein

Query Match 8.6%; Score 183.5; DB 2; Length 629;
Best Local Similarity 26.9%; Pred. No. 0.00074;
Matches 59; Conservative 43; Mismatches 98; Indels 19; Gaps 8;
Qy 19 PFVYLLLIQTDPLEGVNITSPVRLIHGTGKSALLSVQYSTSDRPPVVKQLKRDKPV 78
Db 14 PLLELLM----GLGASGKETPTPTVISMGLGGSVTFSLNISKDAIEHII--WNC---PPKA 65
Qy 79 VVQSIGTEVIGTLRPDYDRIRLFENG-SILLSLQLADEGTYEVEISITDFTTGEXTI 137
Db 66 LALVFPYKDIITLDKNGRLKVEDGYSLYMSNLTKSDSGSYHAQINQKNVILITNKEF 125
Qy 138 NLTVDDVPISRPQVLVASTTVLEL-SEAFLLNCSEHNGTKPS--YTWLKDGKPLNDSRML 194
Db 126 TLHIYKLOKRPQIIVSVTPSDTDSCTFTLICT-VKGTQDSVQYSWTRE-----DTHLN 178
Qy 195 LSPDQKVLITRVLMEDDDLVSCWENPISQGRSLPVKI 233
Db 179 TYDGSHTLRVSQSVQCDPLPYTCKANPVSQNSQPVRI 217

RESULT 12

S34338

Biliary glycoprotein F - mouse

N:Alternate names: mouse hepatitis virus (MHV) receptor glycoprotein

C:Species: Mus musculus (house mouse)

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: S34338; JC1510; A41093

R:Huang, D.C.; Huang, X.F.; Novel, M.; Novel, G.

submitted to the EMBL Data Library, July 1992

A:Description: A Clp-family gene present on the lactose-protease plasmid of lactococcus

A:Reference number: S34338

A:Accession: S34338

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-521 <HUA>

A:Cross-references: UNIPROT:Q61352; EMBL:X67281; NID:g312585; PIDN:CAA47698.1; PID:g3125

R:McCuag, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.

Gene 127, 173-183, 1993

A>Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopro

A:Reference number: JC1505; MUID:93273228; PMID:8500759

A:Accession: JC1510

A:Molecule type: mRNA

A:Residues: 1-81,'Q',83-141,'P',143-521 <MCC>

A:Cross-references: GB:X67281

R:Williams, R.K.; Jiang, G.S.; Holmes, K.V.

Proc. Natl. Acad. Sci. U.S.A. 88, 5533-5536, 1991

A>Title: Receptor for mouse hepatitis virus is a member of the carcinoembryonic antigen

A:Reference number: A41093; MUID:91288498; PMID:1648219

A:Accession: A41093

A>Status: preliminary

A:Molecule type: protein

A:Residues: 35-59 <Wit>

C:Comment: This protein is expressed at the cell surface and plays a determinant role in

C:Genetics:

A:Gene: Bgpf

C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin

C:Keywords: glycoprotein; receptor

F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>

F:160-219/Domain: immunoglobulin homology <IMM1>

F:254-303/Domain: immunoglobulin homology <IMM2>

F:339-396/Domain: immunoglobulin homology <IMM3>

F:87,104,148,199,206,210,226,258,290,304,333,375/Binding site: carbohydrate (Asn) (C

Query Match 8.6%; Score 181.5; DB 2; Length 521;

Best Local Similarity 27.4%; Pred. No. 0.00077;

Matches 52; Conservative 37; Mismatches 84; Indels 17; Gaps 6;

```
Qy 73 RDKPVTVVQSIGTEVIGTLR-----PDYRDRIRLPFENGSLLSLDLQADEGTYEVEISITD 128
Db 69 KGNPVSNAEIVHVTGTNTKTTCPAHSGRBTYVNSGSLIIQRTVKDTGVYIE--WTD 126
Qy 129 DTF--TGSEKINLTVDVPISRPQVLVASTVTLSEAFSLNC--SHENGTRKPSYTWLKDQKP 186
Db 127 ENFRTEATVQFVHQLLKPNITNSNSNPVEGDDSVSLTCDSTYDTPDNITYLWSRNGES 186
Qy 187 LLNDSRMLSPDQKVLITRVLMEDDDLYSQWENPISQGRSLPVKLTIVRRSLY----- 242
Db 187 LSEGRDLKLEGNRTLLTNVTRNDTGPYVCETRNPPVSNRSDPFSLNI-----IYGPDT 241
Qy 243 IILSTGGIFL 252
Db 242 PIISPSDIYL 251

RESULT 13
S41638
N;Alternate names: T-cell surface glycoprotein CD2 precursor - horse
C;Species: Equus caballus (domestic horse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S41638; S31578
R;Tavernor, A.S.; Kydd, J.H.; Bodian, D.L.; Jones, E.Y.; Stuart, D.I.; Davis, S.J.; Butc
R;Tavernor, A.S.; Kydd, J.H.; Bodian, D.L.; Jones, E.Y.; Stuart, D.I.; Davis, S.J.; Butc
A;Title: Expression cloning of an equine T-lymphocyte glycoprotein CD2 cDNA. Structure-b
A;Reference number: S41638; MUID:94155904; PMID:7906650
A;Accession: S41638
A;Molecule type: mRNA
A;Residues: 1-347 <TAV>
A;Cross-references: UNIPROT:P37998; EMBL:X69884; NID:g1057; PIDN:CRAA49511.1; PID:g1058
C;Superfamily: T-cell surface glycoprotein CD2
C;Keywords: Glycoprotein; surface antigen; T-cell; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-347/Product: T-cell surface glycoprotein CD2 #status predicted <MAT>

Query Match 8.5%; Score 180.5; DB 2; Length 347;
Best Local Similarity 26.8%; Pred. No. 0.0053;
Matches 80; Conservative 42; Mismatches 121; Indels 55; Gaps 14;

Qy 101 LFENGSLLSLDLQADEGTYEVEISITDDTFTGKTNLTVDVPISRPQVLVASTVTLLEL 160
Db 81 VLKNGTLKIKHLERHETGYKVDAYDSQKNVLETHLSLELVSKPNISWSCTNT--- 137
Qy 161 SEATFLNCSHENGTKPSYTWLKDQKPLNDSRMLSPDQKVLITRVLMEDDDLYSQWVE 220
Db 138 ---TLTCEVTGKTDFE---LK---LYNGRMIQKSPRKIVYKRASNQIAS-FKCTAN 185
Qy 221 NPISQGRSLPVKITVYRRSSLYII--LSTGGIFLLVTLVTVCACWKPKRQKLEKONS 278
Db 186 NTVSEESSVVRCTEKGDLIYLISGICGGGIIILFVFLALL--IFYISKRK-----KQNS 238
Qy 279 LEYMDQNDRLKPEADTLPRSGEQRKNPMALYILKDKDSPETENPA---PEPRSATEP 335
Db 239 ----RRNDEELEIRAHKV--ISEGRKPHQI-----PGSTPLNPAASQPPPPPSHRP 285
Qy 336 GPPGYSVSPAPVGRSPGLP-IRSAARYPRSPARSPAT-----GRTHSSPPR 380
Db 286 QAPGH--RPQVFGHRPLPGRHVQHQKQRPAPTGTQAOHQKGPPLPRPRVQPKPR 341

RESULT 14
JC1507
Biliary glycoprotein C - mouse
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: JC1507
R;McCuag, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
A;Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopro
A;Reference number: JC1505; MUID:93273228; PMID:8500759
A;Accession: JC1507
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A;Molecule type: mRNA
A;Residues: 1-278 <MCC>
A;Cross-references: UNIPROT:Q61350; GB:X67278
C;Comment: This protein is expressed at the cell surface and plays a determinant role in
C;Genetics:
A;Gene: Bgpc
C;Superfamily: Biliary glycoprotein; carcinoembryonic antigen precursor amino-terminal h
C;Keywords: glycoprotein; receptor
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;138-214/Domain: immunoglobulin homology <IMM1>
F;159-216/Domain: immunoglobulin homology <IMM2>
F;71,89,104,153,195/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 8.5%; Score 179.5; DB 2; Length 278;
Best Local Similarity 31.7%; Pred. No. 0.00046;
Matches 45; Conservative 29; Mismatches 63; Indels 5; Gaps 4;

Qy 95 YRDRIRLFENGSLLSLDLQADEGTYEVEISITDDTF--TGKTNLTVDVPISRPQVLVA 153
Db 95 YSGREIIVNSGSLLFQMITMKDMGVVTLD--MTDENYRRTQATVRFHVHQVTPQFLQVT 152
Qy 154 STTVLSEAFNLNCSHENGTRKPSYTWLKDQKPLNDSRMLSPDQKVLITRVLMEDDDD 213
Db 153 NTTVKEL-DSVTLTCL--SNDIGANIQWLFNFSQSLQTLRMTLSQNNSLRIDPIKREDAG 210
Qy 214 LYSQWENPISQGRSLPVKITV 235
Db 211 EYOCESINPVSRRSNIKLDI 232

RESULT 15
A54879
Pregnancy-specific glycoprotein rncGM3 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C;Accession: A54879
R;Chen, H.; Chen, C.L.; Chou, J.Y.
Biochemistry 33, 9615-9626, 1994
A;Title: Characterization of two promoters of a rat pregnancy-specific glycoprotein gene
A;Reference number: A54879; MUID:94347731; PMID:8068638
A;Accession: A54879
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-475 <CHE>
A;Cross-references: UNIPROT:Q62664; GB:U09815; NID:g497254; PIDN:AAA56870.1; PID:g497255
A;Note: authors translated the codon GCT for residue 64 as Gly
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: glycoprotein
F;1-137/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA1>
F;242-378/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA2>
F;399-456/Domain: immunoglobulin homology <IMM2>

Query Match 8.4%; Score 178.5; DB 2; Length 475;
Best Local Similarity 31.5%; Pred. No. 0.0011;
Matches 67; Conservative 26; Mismatches 105; Indels 15; Gaps 8;

Qy 29 DPLEGVNITSPVRLIHGTGCKSALLSVQYSTSSDRPVKWK-----QLKRDKPVTVVQSI 83
Db 269 DPVTSVPLMEIPVRHAGEVESVLLYVH--NLPEALQTFWSYKGVSLKEPK--IAEYSI 324
Qy 84 GTEVIGTLRPDYRDIRLRFENGSLLSLDLQADEGTYEVEISITDDTFTGKTNLTVDV 143
Db 325 ATKSVFP-CPAHRGRATGYTNGSLLLQLDLTARDTGLYTL-VTLDSNSKIKSAPVQVTVHK 382
Qy 144 PISRPQVLVASTTV--LELSEAFNLNCSHENGTRKPSYTWLKDQKPLNDSRMLSPDQKVL 202
Db 383 PVTQPFRLVTESTVTVQSSVVFT--CLUSDN-TGVSIKRLFKQNQLQVTERMTLSFSPNCQL 439
Qy 203 TITRVLMEDDDLYSQWENPISQGRSLPVKITV 235
Db 440 RIHDVREDAGQVRCFAFNFISSKTSRPVSLAV 472
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Search completed: July 26, 2005, 16:14:14
Job time : 25.0385 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2005, 15:57:23 ; Search time 106.504 Seconds
(without alignments)
2000.159 Million cell updates/sec

Title: US-10-706-691-16

Perfect score: 2122

Sequence: 1 MKRERGALSRSRALRLAPF.....TAGVHIIRQDEAGPVEISA 416

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2118	99.8	416	2 QN7I3	QN7I3 homo sapien
2	2114	99.6	416	2 Q67IP8	Q67IP8 homo sapien
3	1967	92.7	413	2 Q640R3	Q640R3 mus musculus
4	1478.5	69.7	367	2 Q6ZWL4	Q6ZWL4 homo sapien
5	854.5	40.3	165	2 Q6ND35	Q6ND35 homo sapien
6	282	13.3	450	2 Q6UXIO	Q6UXIO homo sapien
7	224	10.6	350	2 Q6SZ59	Q6SZ59 cercocebus
8	221	10.4	351	1 C02 HUMAN	P06729 homo sapien
9	217.5	10.2	345	2 Q6SZ58	Q6SZ58 macaca assa
10	215.5	10.2	344	2 Q6SZ62	Q6SZ62 papio anubi
11	215	10.1	345	2 Q6SZ63	Q6SZ63 pan troglod
12	212.5	10.0	334	2 Q6SZ56	Q6SZ56 macaca mme
13	212.5	10.0	341	2 Q6SZ57	Q6SZ57 macaca arct
14	211	9.9	341	2 Q61354	Q61354 mus musculus
15	210.5	9.9	292	2 Q6UY47	Q6UY47 homo sapien
16	210.5	9.9	351	2 Q6SZ61	Q6SZ61 macaca fasc
17	207.5	9.8	351	2 Q6SZ60	Q6SZ60 macaca mula
18	202.5	9.5	278	2 Q6Z332	Q6Z332 mus musculus
19	202.5	9.5	340	2 Q61349	Q61349 mus musculus
20	199.5	9.4	1093	1 LIG1 HUMAN	Q96JAL homo sapien
21	197.5	9.3	352	2 Q91W66	Q91W66 mus musculus
22	197.5	9.3	365	1 CXAR MOUSE	P97792 mus musculus
23	197.5	9.3	365	2 Q9WMV3	Q9WMV3 bos taurus
24	197.5	9.3	365	2 Q9DBJ8	Q9DBJ8 mus musculus
25	196.5	9.3	319	1 A33 HUMAN	Q99795 homo sapien
26	196.5	9.3	387	2 Q86XK7	Q86XK7 homo sapien
27	196.5	9.3	412	2 Q6MZS4	Q6MZS4 homo sapien
28	194	9.1	328	2 Q6FHAB	Q6FHAB homo sapien
29	193	9.1	328	2 O15430	O15430 homo sapien
30	189.5	8.9	235	2 O75296	O75296 homo sapien
31	189.5	8.9	345	2 Q9UIB8	Q9UIB8 homo sapien

32	189	8.9	272	2 Q8RLN5	Q8RLN5 mus musculus
33	188.5	8.9	1091	1 LIG1 MOUSE	P70193 mus musculus
34	187.5	8.8	325	2 Q95751	Q95751 homo sapien
35	187.5	8.8	533	2 Q8NCB6	Q8NCB6 homo sapien
36	187	8.8	344	2 Q9R067	Q9R067 rattus norv
37	187	8.8	358	2 Q9R066	Q9R066 rattus norv
38	187	8.8	365	1 CXAR HUMAN	P78310 homo sapien
39	186.5	8.8	327	2 Q96IQ7	Q96IQ7 homo sapien
40	186	8.8	310	2 Q68FQ2	Q68FQ2 rattus norv
41	186	8.8	337	2 P97268	P97268 cavia porce
42	186	8.8	341	2 Q61353	Q61353 mus musculus
43	186	8.8	365	2 Q6VAN5	Q6VAN5 bos taurus
44	186	8.8	372	2 Q6VAN6	Q6VAN6 bos taurus
45	186	8.8	388	2 Q8NC34	Q8NC34 homo sapien

ALIGNMENTS

RESULT 1

Q8N7I3

ID Q8N7I3 PRELIMINARY; PRT; 416 AA.

AC Q8N7I3;

DT 01-OCT-2002 (Tremblrel. 22, Created)

DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)

DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

DE Hypothetical protein FLJ25530.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,

RA Fukuzumi Y., Fujimori Y., Komiyama M., Suzuki Y., Hata H.,

RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,

RA Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,

RA Negai K., Isogai T., Sugano S.,

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK098396; BAC05297.1; -

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003598; IG_c2.

DR Pfam; PF00047; ig; 1.

DR SMART; SM00408; IGc2; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

SQ SEQUENCE 416 AA; 45994 MW; 47120CA9A00EE1CF CRC64;

Query Match 99.8%; Score 2118; DB 2; Length 416;

Best Local Similarity 99.8%; Pred. No. 1.1e-114;

Matches 415; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKRERGALSRSRALRLAPFVYLLLIQTDPLEGVNTSPVRLIHGTGKSALLSVQYSST 60

Db 1 MKRERGALSRSRALRLAPFVYLLLIQTDPLEGVNTSPVRLIHGTGKSALLSVQYSST 60

Qy 61 SSDPVPVVKQIKRDPKVTYVQSIGTEVIGTLRPDYRDIRLFENGSLLLDLQADEGTY 120

Db 61 SSDPVPVVKQIKRDPKVTYVQSIGTEVIGTLRPDYRDIRLFENGSLLLDLQADEGTY 120

Qy 121 EVELSIITDDFTFGKTIINLTVDVPIRSPQVLVASTTVLELSEAFILNCSHENGTKPSYTW 180

Db 121 EVELSIITDDFTFGKTIINLTVDVPIRSPQVLVASTTVLELSEAFILNCSHENGTKPSYTW 180

Qy 181 LKDGKPLNDSRMLLSPDKVLTITRVLMEDDDDLYSCWVENPISQGRSLPKVITVYRRSS 240

Db 181 LKDGKPLNDSRMLLSPDKVLTITRVLMEDDDDLYSCWVENPISQGRSLPKVITVYRRSS 240

Qy 241 LYIILSTGGIFLLVTLVTVCACWKPSRKKQKLEKQNSLEYMDQNDRLKPEADTLPRSG 300

Db 241 LYIILSTGGIFLLVTLVTVCACWKPSRKKQKLEKQNSLEYMDQNDRLKPEADTLPRSG 300

Qy 301 EQERKNPMALYILKDKDSPETEENPAPEPRSATPPGPGYSVSPAVPGSRPGLPIRSARR 360

Db 301 EQERKNPMALYILKDKSPETEENPAPEPRSPATEPGPGYSVSPAVPGRSPGLPIRSARR 360
Qy 361 YPRSPARSPATGRTHSSPPRAPSPGGRSASRTLRTAGVHIIREQDEAGPVEISA 416
Db 361 YPRSPARSPATGRTHSSPPRAPSPGGRSASRTLRTAGVHIIREQDEAGPVEISA 416

RESULT 2
Q67IP8 PRELIMINARY; PRT; 416 AA.
AC Q67IP8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Shen S., Moh M.C.;
RL "A gene related to human hepatocellular carcinoma.";
DR EMBL; AY047587; AAQ93018.1; -;
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Hypothetical protein.
SQ SEQUENCE 416 AA; 46055 MW; 7B8882298BEB4ABF CRC64;

Query Match 99.6%; Score 2114; DB 2; Length 416;
Best Local Similarity 99.5%; Pred. No. 1.9e-114;
Matches 414; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKRERGALSASRALRALAPFYVLLLIQTDPLEGVNITSPVRLIHGTGKSGALLSVQYSST 60
Db 1 MERERGALSASRALRALAPFYVLLLIQTDPLEGVNITSPVRLIHGTGKSGALLSVQYSST 60
Qy 61 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFPENGSLLLSDQLADEGTY 120
Db 61 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFPENGSLLLSDQLADEGTY 120
Qy 121 EVEISITDDTFTGKTIINLTVDVPISRPOVLVASTVTLSEAFTLNCSHENGKPSVTW 180
Db 121 EVEISITDDTFTGKTIINLTVDVPISRPOVLVASTVTLSEAFTLNCSHENGKPSVTW 180
Qy 181 LKDGKPLNDSRMLSPDQKVLITRVLMEDDDLSCMVENPISQGRSLPKIIVYRRSS 240
Db 181 LKDGKPLNDSRMLSPDQKVLITRVLMEDDDLSCMVENPISQGRSLPKIIVYRRSS 240
Qy 241 LYIILSTGGIFLLVTLVTVCAWPKSRKKQKLEKQNSLEYMDNDRLKPEADTLPRSG 300
Db 241 LYIILSTGGIFLLVTLVTVCAWPKSRKKQKLEKQNSLEYMDNDRLKPEADTLPRSG 300
Qy 301 EOERKNPMALYILKDKSPETEENPAPEPRSPATEPGPGYSVSPAVPGRSPGLPIRSARR 360
Db 301 EOERKNPMALYILKDKSPETEENPAPEPRSPATEPGPGYSVSPAVPGRSPGLPIRSARR 360
Qy 361 YPRSPARSPATGRTHSSPPRAPSPGGRSASRTLRTAGVHIIREQDEAGPVEISA 416
Db 361 YPRSPARSPATGRTHSSPPRAPSPGGRSASRTLRTAGVHIIREQDEAGPVEISA 416

RESULT 3
Q64OR3 PRELIMINARY; PRT; 413 AA.
ID Q64OR3

AC Q64OR3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 2900042E01RIK protein (Fragment).
GN Name=2900042E01RIK;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klauser R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh F.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszewski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Director MGC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC082537; AA82537.1; -;
FT NON TER 1
SQ SEQUENCE 413 AA; 45665 MW; B6EFCAD6D2CA3C1 CRC64;

Query Match 92.7%; Score 1967; DB 2; Length 413;
Best Local Similarity 94.2%; Pred. No. 6.1e-106;
Matches 389; Conservative 10; Mismatches 12; Indels 2; Gaps 1;

Qy 6 GALSRSALRALAPFYVLLLIQTDPLEGVNITSPVRLIHGTGKSGALLSVQYSSTSDRP 65
Db 1 GALSRSALRALAPFYVLLLIQTDPLEGVNITSPVRLIHGTGKSGALLSVQYSSTSDRP 60
Qy 66 VVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFPENGSLLLSDQLADEGTYEVS 125
Db 61 VVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFPENGSLLLSDQLADEGTYEVS 120
Qy 126 ITDDTFTGKTIINLTVDVPISRPOVLVASTVTLSEAFTLNCSHENGKPSYTWLKDCK 185
Db 121 ITDDTFTGKTIINLTVDVPISRPOVLVASTVTLSEAFTLNCSHENGKPSYTWLKDCK 180
Qy 186 PLLNDSRMLSPDQKVLITRVLMEDDDLSCMVENPISQGRSLPKIIVYRRSSLIIL 245
Db 181 PLLNDSRMLSPDQKVLITRVLMEDDDLSCMVENPISQGRSLPKIIVYRRSSLIIL 240
Qy 246 STGGIFLLVTLVTVCAWPKSRKKQKLEKQNSLEYMDNDRLKPEADTLPRSGEQE 303
Db 241 STGGIFLLVTLVTVCAWPKSRKKQKLEKQNSLEYMDNDRLKPEADTLPRSGEQE 300
Qy 304 RKQPMALYILKDKSPETEENPAPEPRSPATEPGPGYSVSPAVPGRSPGLPIRSARYPR 363
Db 301 RKQPMALYILKDKSPETEENPAPEPRSPATEPGPGYSVSPAVPGRSPGLPIRSARYPR 360
Qy 364 SPARSPATGRTHSSPPRAPSPGGRSASRTLRTAGVHIIREQDEAGPVEISA 416

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Db 361 SPARSPATGRTHTPPRAPSPGRRSSSRSLRTAGVQIRIQDESGQVEISA 413
RESULT 4
Q6ZWL4 PRELIMINARY; PRT; 367 AA.
AC Q6ZWL4;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Hypothetical protein FLJ16002.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,
RA Matsumura Y., Moriya S., Chiba E., Momiyama H., Onogawa S.,
RA Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Kataoka R.,
RA Kuga N., Kuroda A., Saoh I., Kanata K., Takami S., Terashima Y.,
RA Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T.,
RA Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K.,
RA Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y.,
RA Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuno Y., Nagai K., Isogai T.,
RA Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK122595; BAC85486.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG 1.
DR SMART; SM00409; IG 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Receptor.
SQ SEQUENCE 367 AA; 40456 MW; 35956FA245A408F0 CRC64;
Query Match 69.7%; Score 1478.5; DB 2; Length 367;
Best Local Similarity 84.7%; Pred. No. 9.5e-78;
Matches 305; Conservative 12; Mismatches 26; Indels 17; Gaps 4;
Qy 1 MKRERGALSRSALRLAPFYVLLLIQTDPLEGVNIITSPVRLIHGTGKSGALLSVQYSST 60
Db 1 MKRERGALSRSALRLAPFYVLLLIQTDPLEGVNIITSPVRLIHGTGKSGALLSVQYSST 60
Qy 61 SSDRPVVKWQIKRDKPVTWQSIGTEVIGTLRPDPRDRIRLFENGSLLLSDQLADRGTY 120
Db 61 SSDRPVVKWQIKRDKPVTWQSIGTEVIGTLRPDPRDRIRLFENGSLLLSDQLADRGTY 120
Qy 121 EVELISITDDFTGKTLNLTVDVPIRSPQVLVASTTVEILSEAFLLNCSHENGTPKPSYTW 180
Db 121 EVELISITDDFTGKTLNLTVDVPIRSPQVLVASTTVEILSEAFLLNCSHENGTPKPSYTW 180
Qy 181 LKDGKPLNDSRMLLSPDKVLTITRVLMDDEDDLYSCWVENPISQGRSLPKVITVYRRSS 240
Db 181 LKDGKPLNDSRMLLSPDKVLTITRVLMDDEDDLYSCWVENPISQGRSLPKVITVYRRSS 240
Qy 241 LYILSTGGIFLLVTLVTVCAWKPSKRRKKLEKQNSLEYMDQNDRLKPEADTLPRSG 300
Db 241 LYILSTGGIFLLVTLVTVCAWKPSKRRKKLEKQNSLEYMDQNDRLKPEADTLPRSG 300
Qy 301 EQERKNPMALYI-----LKDQSDPETEENPAPEPRSPATEPGPPGYSVSPVPGR 349
Db 299 ----QSPITSRVSGCWKEAKELGDKENSSAGTLPDGLGASKGKEPEPASLASHSLPRR 354
RESULT 5
Q8ND35
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Q8ND35 PRELIMINARY; PRT; 165 AA.
Q8ND35;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Hypothetical protein DKFZp5470159 (Fragment).
GN Name=DKFZp5470159;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Bloeker H., Boscher M., Brandt P., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834419; CAD39081.1; -.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 165 AA; 18161 MW; 5052FA978C437486 CRC64;
Query Match 40.3%; Score 854.5; DB 2; Length 165;
Best Local Similarity 99.4%; Pred. No. 4.3e-42;
Matches 165; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 251 FLIVTLTVTVCAWKPSKRRKKLEKQNSLEYMDQNDRLKPEADTLPRSGQERKNPMAL 310
Db 1 FLIVTLTVTVCAWKPSKRRKKLEKQNSLEYMDQNDRLKPEADTLPRSGQERKNPMAL 59
Qy 311 YILKQSDPETEENPAPEPRSPATEPGPPGYSVSPVPGRSPGLPFRSARRYPSPARSPA 370
Db 60 YILKQSDPETEENPAPEPRSPATEPGPPGYSVSPVPGRSPGLPFRSARRYPSPARSPA 119
Qy 371 TGRTHSSPPRAPSPGRRSSASRTLRTAGVHIIRIQDEAGPVEISA 416
Db 120 TGRTHSSPPRAPSPGRRSSASRTLRTAGVHIIRIQDEAGPVEISA 165
RESULT 6
Q6UXIO PRELIMINARY; PRT; 450 AA.
AC Q6UXIO;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE WLKV305.
GN ORFNames=UNQ305;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vanden R., Watanabe C., Wiewand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AV358345; AAC88711.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG 1.
DR SMART; SM00409; IG; 3.
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SEQUENCE FROM N.A.
 RC TISSUE-Pancreas, and Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Klausner R.D., Felling B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Hopkins R.F., Jordan H., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bobak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smal M.A.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 25-206.
 RX MEDLINE=95086863; PubMed=7994575;
 RA Bodian D.L., Jones E.Y., Harlos K., Stuart D.I., Davis S.J.;
 RA "Crystal structure of the extracellular region of the human cell
 RT adhesion molecule CD2 at 2.5-A resolution";
 RL Structure 2:755-766 (1994).
 RN [10]
 RP STRUCTURE BY NMR OF 25-129.
 RX MEDLINE=94348865; PubMed=7915183; DOI=10.1016/0969-2126(93)90009-6;
 RA Withka J.M., Wyss D.F., Wagner G., Arulanandam A.R.N., Reinherz E.D.,
 RA Recny M.A.;
 RT "Structure of the glycosylated adhesion domain of human T lymphocyte
 RT glycoprotein CD2";
 RL Structure 1:69-81 (1993).
 RN [11]
 RP STRUCTURE BY NMR OF 25-129.
 RX MEDLINE=95381065; PubMed=7544493;
 RA Wyss D.F., Choi J.S., Li J., Knoppers M.H., Willis K.J.,
 RA Arulanandam A.R., Smolyar A., Reinherz E.L., Wagner G.;
 RT "Conformation and function of the N-linked glycans in the adhesion
 RT domain of human CD2";
 RL Science 269:1273-1278 (1995).
 RN [12]
 RP MUTAGENESIS.
 RX MEDLINE=88039075; PubMed=2444890; DOI=10.1038/329842a0;
 RA Peterson A., Seed B.;
 RA "Monoclonal antibody and ligand binding sites of the T cell
 RT erythrocyte receptor (CD2).";
 RL Nature 329:842-846 (1987).
 RN [13]
 RP CD59-BINDING DATA.
 RX MEDLINE=92311658; PubMed=1377404;
 RA Hahn W.C., Menu E., Bothwell A.L.M., Sims P.J., Bierer B.E.;
 RA "Overlapping but nonidentical binding sites on CD2 for CD58 and a
 RT second ligand CD59";
 RL Science 256:1805-1807 (1992).
 CC -!- FUNCTION: CD2 interacts with lymphocyte function-associated
 CC antigen (LFA-3) and CD48/ICAM1 to mediate adhesion between T cells
 CC and other cell types. CD2 is implicated in the triggering of T-
 CC cells, the cytoplasmic domain is implicated in the signaling
 CC function.
 CC -!- SUBUNIT: Interacts with CD2AP (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -!- DATABASE: NAME=PRO; NCBI=cd guide CD2 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd2.htm".
 CC -----

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 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

 CC EMBL; M16445; AAA51738.1; -
 CC EMBL; M14362; AAA35571.1; -
 CC EMBL; M16336; AAA51946.1; -
 CC EMBL; M19806; AAA53095.1; -
 CC EMBL; M19798; AAA53095.1; JOINED.
 CC EMBL; M19800; AAA53095.1; JOINED.
 CC EMBL; M19802; AAA53095.1; JOINED.
 CC EMBL; M19804; AAA53095.1; JOINED.
 CC EMBL; X07871; CAA30721.1; -
 CC EMBL; X07872; CAA30721.1; JOINED.
 CC EMBL; X07873; CAA30721.1; JOINED.
 CC EMBL; X07874; CAA30721.1; JOINED.
 CC EMBL; AL135798; CAC14840.1; -
 CC EMBL; BC033583; AAH33583.1; -
 CC PIR; A28967; RWIUC2.
 CC PDB; 1CDB; NMR; @=25-129.
 CC PDB; 1GFA; NMR; @=25-129.
 CC PDB; 1HNF; X-ray; @=25-206.
 CC PDB; 1L22; NMR; B=294-304.
 CC GlycoSuiteDB; P06729; -
 CC Genew; HGNC:1639; CD2.
 CC H-invDB; HIX0000931; -
 CC MIM; 186990; -
 CC GO; GO:0005887; C:integral to plasma membrane; NAS.
 CC GO; GO:0005515; F:protein binding; IPI.
 CC GO; GO:0004872; F:receptor activity; NAS.
 CC GO; GO:0007166; P:cell surface receptor linked signal transdu. . . ; TAS.
 CC GO; GO:0016337; P:cell-cell adhesion; NAS.
 CC GO; GO:0006917; P:induction of apoptosis; TAS.
 CC GO; GO:0001766; P:lipid raft polarization; TAS.
 CC GO; GO:0030101; P:natural killer cell activation; NAS.
 CC GO; GO:0030887; P:positive regulation of dendritic cell activ. . . ; NAS.
 CC GO; GO:0045580; P:regulation of T-cell differentiation; NAS.
 CC GO; GO:0042110; P:T-cell activation; TAS.
 CC InterPro; IPR008424; CD2.
 CC InterPro; IPR007110; Ig-like.
 CC Pfam; PF05790; CD2; 1.
 CC PROSITE; PS50835; IG_LIKE; FALSE NEG.
 CC 3D-structure; Antigen; Cell adhesion; Glycoprotein; T-cell;
 CC Immunoglobulin domain; Polymorphism; Repeat; Signal; T-cell;
 CC Transmembrane.
 CC SIGNAL 1 24
 CC CHAIN 25 351 T-cell surface antigen CD2.
 CC DOMAIN 25 209 Extracellular (Potential).
 CC TRANSMEM 210 235 Potential.
 CC DOMAIN 236 351 Cytoplasmic (Potential).
 CC DOMAIN 25 128 Ig-like V-type.
 CC DOMAIN 129 209 Ig-like C2-type.
 CC DOMAIN 61 75 LFA-3 (CD58) binding region 1.
 CC DOMAIN 106 120 LFA-3 (CD58) binding region 2.
 CC DOMAIN 282 338 Pro-rich.
 CC DISULFID 139 203 By similarity.
 CC DISULFID 146 186 By similarity.
 CC CARBOHYD 89 89 N-linked (GLCNAC. . .) (Potential).
 CC CARBOHYD 141 141 N-linked (GLCNAC. . .) (Potential).
 CC CARBOHYD 150 150 N-linked (GLCNAC. . .) (Potential).
 CC VARIANT 266 266 Q -> H (in dbSNP:699738).
 CC FT MUTAGEN 67 67 FTID=VAR_017104.
 CC FT MUTAGEN 70 70 K->R: Loss of LFA-3 binding.
 CC FT MUTAGEN 110 110 Q->K: Loss of LFA-3 binding.
 CC FT MUTAGEN 111 111 Y->D: Loss of LFA-3 and CD59 binding.
 CC FT MUTAGEN 111 111 D->H: Loss of LFA-3 and CD59 binding.
 CC Query Match 10.4%; Score 221; DB 1; Length 351;
 CC Best Local Similarity 22.9%; Pred. No. 4.8e-05;
 CC Matches 85; Conservative 60; Mismatches 164; Indels 62; Gaps 12;

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QY 17 LAPFVYLLIQTDLLEGWITSPVRLIHGTGKSAALLSVQYSSSTSDRPVVKWQKLRDKP 76
D 8 VASPELLFNSSKAGVSKBITNALE-TWGALGQDINLDIPSFQMSDDIDDKWEKTSK- 65
QY 77 VTVVQSIGTEVIGTLRPD-----YRDIRLFPENGSLLLSDQLADEGTYEVEISITDDTF 131
D 66 -----KKIAQFRKEKETFKEKDYKLPKNGTLAKHLKTDQDIYKSVIYDTGKN 116
QY 132 TGEKTINLTVDVPIRSQVLTSLSEAFNLCSHENGTKPSYTWLKDGPPLNDS 191
D 117 VLEKIFDLKIQERVSKPKI---SWTCINT-----TLTCEVMNGTDPNLNLYQDGKHLKLSQ 169
QY 192 RMLLSPQKVLITIRVLMEDDDLSCWVENPISQGRSLPVKITVYRRSSLYIILS-TGGI 250
D 170 RVITHKWTTSLSAK-----FKTAGNKSKESSVEPVSCPEKGLDIYLIIGICGG 220
QY 251 FLLVTLVTVCACWKPSKRKQKLEKQNSLEYMDQNDRLKPEADTLPRSGEQERKNPMAL 310
D 221 SLLMVFVALLVFIYITKRKQRS-----RRNDELETRAH---RVATEERGRKPQ 267
QY 311 YILKQDSPETENPAPRSPATE-----PGPGYSVS-----PAVPG-----RSPGLP 354
D 268 IPASTPQNPAATSOHPPPGHRSPQAPSHRPPPGHVRHQPKRPPAPSGTQVHQKQKGP 327
QY 355 IRSARRYPSP 365
D 328 LPRPRVQPKPP 338
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RESULT 9

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Q6SZ58 PRELIMINARY; PRT; 345 AA.
ID Q6SZ58
AC Q6SZ58;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DE Cluster of differentiation 2 (Fragment).
GN Name=CD2;
OS Macaca assamensis (Assam's macaque) (Assam's monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9551;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15302161;
RA Damschroder M.M., Kozhich A.A., Woods R.M., Cheng L., Mullikin B.A.,
RA Wilson S.D., Ulbrandt N.D., Bachy C.M., Wu H., Suzich J.A.,
RA Kiener P.A., Dall'Acqua W.F., White W.I.;
RT "Analysis of human and primate CD2 molecules by protein sequence and
RT epitope mapping with anti-human CD2 antibodies.";
RL Mol. Immunol. 41:985-1000(2004).
DR EMBL; AY445039; AAR15886.1; -.
DR HSP; P08921; IAG4.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008424; CD2.
DR Pfam; PF05790; C2-set; 1.
FT NON TER 345
SQ SEQUENCE 345 AA; 38952 MW; 063DF110344542A7 CRC64;
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Query Match 10.2%; Score 217.5; DB 2; Length 345;
Best Local Similarity 23.3%; Pred. No. 7.6e-05;
Matches 80; Conservative 54; Mismatches 148; Indels 61; Gaps 11;

QY 45 GTVCKSALLSVQYSSSTSDRPVVKWQKLRDKPVTVQSIGTEVIGTLRP-----DYDR 99
D 35 GALGQDIDLIPSFQMSDDIDDKWEKTSK-----KKIAQFRKEKETEEDKDAY 84
QY 100 RLFENGSLLLSDQLADEGTYEVEISITDDTFTEKTIINLTVDVPIRSQVLTSLSEAFNLCSHENGTKPSYTWLKDGPPLNDS 159
D 85 KLFKNGTLKIKHLKIHODDSYKSVIYDTGKGVLEKTFDLKIQERVSEPKI---SWTCIN 141
QY 160 LSEAFNLCSHENGTKPSYTWLKDGPPLNDSRMLSPDQKVLITIRVLMEDDDLSCW 219
D 142 T-----TLTCEVMNGTDPNLNLYQDGKHLKLSQRIYTHKWTTSLSAK-----FKCTA 188
QY 220 ENPISQGRSLPVKITVYRRSSLYIILS-TGGIFLLVTLVTVCACWKPSKRKQKLEKQNS 278
D 189 GNVKSKESRMETVSCPEKGLDIYLIIGICGGSLMVFVALLVFIYITKRKQRS----- 242
QY 279 LEYMDQNDRLKPEADTLPRSGEQERKNPMALYILKQDSPETENPAPRSPATE----- 334
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D 85 KLFKNGTLKIKHLKIHODDSYKSVIYDTGKGVLEKTFDLKIQERVSEPKI---SWTCIN 141
QY 160 LSEAFNLCSHENGTKPSYTWLKDGPPLNDSRMLSPDQKVLITIRVLMEDDDLSCW 219
D 142 T-----TLTCEVMNGTDPNLNLYQDGKHLKLSQRIYTHKWTTSLSAK-----FKCTA 188
QY 220 ENPISQGRSLPVKITVYRRSSLYIILS-TGGIFLLVTLVTVCACWKPSKRKQKLEKQNS 278
D 189 GNVKSKESRMETVSCPEKGLDIYLIIGICGGSLMVFVALLVFIYITKRKQRS----- 242
QY 279 LEYMDQNDRLKPEADTLPRSGEQERKNPMALYILKQDSPETENPAPRSPATE----- 334
D 243 -----QRNDELETRAH---RVATEERGRKPHQIPASTPQNPAASQHPPPGHRSPQAPSH 295
QY 335 -PGPGYSVS-----PAVPG-----RSPGLPIRSARRYPSP 365
D 296 RPLPPGHRVQHQPKRPPAPSGTQVHQKQKGPPLPRPRVQPKPP 338
```

RESULT 10

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Q6SZ62 PRELIMINARY; PRT; 344 AA.
ID Q6SZ62
AC Q6SZ62;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DE Cluster of differentiation 2 (Fragment).
GN Name=CD2;
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15302161;
RA Damschroder M.M., Kozhich A.A., Woods R.M., Cheng L., Mullikin B.A.,
RA Wilson S.D., Ulbrandt N.D., Bachy C.M., Wu H., Suzich J.A.,
RA Kiener P.A., Dall'Acqua W.F., White W.I.;
RT "Analysis of human and primate CD2 molecules by protein sequence and
RT epitope mapping with anti-human CD2 antibodies.";
RL Mol. Immunol. 41:985-1000(2004).
DR EMBL; AY445035; AAR15882.1; -.
DR HSP; P08921; IAG4.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008424; CD2.
DR Pfam; PF05790; C2-set; 1.
FT NON TER 344
SQ SEQUENCE 344 AA; 38916 MW; 063CF2A3869E5BA6 CRC64;
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Query Match 10.2%; Score 215.5; DB 2; Length 344;
Best Local Similarity 23.3%; Pred. No. 9.8e-05;
Matches 80; Conservative 54; Mismatches 148; Indels 61; Gaps 11;

QY 45 GTVCKSALLSVQYSSSTSDRPVVKWQKLRDKPVTVQSIGTEVIGTLRP-----DYDR 99
D 35 GALGQDIDLIPSFQMSDDIDDKWEKTSK-----KKIAQFRKEKETEEDKDAY 84
QY 100 RLFENGSLLLSDQLADEGTYEVEISITDDTFTEKTIINLTVDVPIRSQVLTSLSEAFNLCSHENGTKPSYTWLKDGPPLNDSRMLSPDQKVLITIRVLMEDDDLSCW 159
D 85 KLFKNGTLKIKHLKIHODDSYKSVIYDTGKGVLEKTFDLKIQERVSEPKI---SWTCIN 141
QY 160 LSEAFNLCSHENGTKPSYTWLKDGPPLNDSRMLSPDQKVLITIRVLMEDDDLSCW 219
D 142 T-----TLTCEVMNGTDPNLNLYQDGKHLKLSQRIYTHKWTTSLSAK-----FKCTA 188
QY 220 ENPISQGRSLPVKITVYRRSSLYIILS-TGGIFLLVTLVTVCACWKPSKRKQKLEKQNS 278
D 189 GNVKSKESRMETVSCPEKGLDIYLIIGICGGSLMVFVALLVFIYITKRKQRS----- 242
QY 279 LEYMDQNDRLKPEADTLPRSGEQERKNPMALYILKQDSPETENPAPRSPATE----- 334
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Db 243 ----RRNDELEIRAH---RVATEERGRKHQIPASTPONPAASQHPPPPGRHQAPSH 295
Qy 335 -PGPPGYSVS-----PAVPG-----RSPGLPIRSARYPRSP 365
Db 296 RPLPPGHRVQHQPQRPPAPSGTQVHQKGGPLPRPRVQPKPP 338

RESULT 11
Q6SZ63
ID Q6SZ63 PRELIMINARY; PRT; 345 AA.
AC Q6SZ63;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Cluster of differentiation 2 (Fragment).
GN Name=CD2;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15302161;
RA Damschroder M.M., Kozhich A.A., Woods R.M., Cheng L., Mullikin B.A.,
RA Wilson S.D., Ulbrandt N.D., Bachy C.M., Wu H., Suzich J.A.,
RA Kiener P.A., Dall'Acqua W.F., White W.I.;
RT "Analysis of human and primate CD2 molecules by protein sequence and
RT epitope mapping with anti-human CD2 antibodies.";
RL Mol. Immunol. 41:985-1000(2004).
DR EMBL; AY445034; AARI5881.1; -.
DR HSP; P08921; IAG4.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0007155; P: cell adhesion; IEA.
DR InterPro; IPR008424; CD2.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF05790; C2-set; 1.
FT NON TER 345
SQ SEQUENCE 345 AA; 38833 MW; 6B23B5AC3A57C3C7 CRC64;

Query Match 10.1%; Score 215; DB 2; Length 345;
Best Local Similarity 22.6%; Pred. No. 0.00011;
Matches 84; Conservative 60; Mismatches 165; Indels 62; Gaps 12;

Qy 17 LAPFVLLLIOTDPLEGVNITSPVRLIHGTGKSSALLSVQYSSTSSDRPVVKWQKRDKP 76
Db 8 VASFLIFNVSKGAVSEITNABE-TWAGLQDINLDIPFQMSDDIDDKWETSCK- 65
Qy 77 VTVQSIGTEVIGTLRPD-----YRDLRLFENGSLLSLDLQADGTYVEISITDDTF 131
Db 66 -----KKIAQFRKEKTFKEKDYKLFKNGTLKIKHLKTDQDIYKYSIVDTGKN 116
Qy 132 TGEKTNITVDVPIRSPQVLVASTVLELSAFTLNCSHENGTKPSYTLWKDGPLLND 191
Db 117 VLEKIFDLKIQRVSKPKI---SWTCINT---TLTCEVMNGTDPFLNLYQDGKHLK 169
Qy 192 RMLSPDQKVLITITVLMDDDLLSCMVENPISQGRSLPVKITVYRRSSLYIILS-TGGI 250
Db 170 RVITHKWTISAK-----FKTAGNKVSKESSEVPVSCPEKGLDIYLIIGICGG 220
Qy 251 FLVTLTVTCACWKPSKRKQKLEKQNSLEYMDQNDRLKPEADTLPRSGQERKNPMAL 310
Db 221 SLLVVFALLVYITKRKQKS-----RRNDELETRAH---RVATEERGRKHQ 267
Qy 311 YILKDKSPETEENPAPPSATE-----PGPPGYSVS-----PAVPG-----RSPGLP 354
Db 268 IPASTPONPAASQHPPPPGRHQAPSHRPPPPGHRVQHQPQRPPAPSGTQVHQKGGP 327
Qy 355 IRSARYPRSP 365
Db 328 LPRPRVQPKPP 338

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RESULT 12
Q6SZ56
ID Q6SZ56 PRELIMINARY; PRT; 334 AA.
AC Q6SZ56;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Cluster of differentiation 2 (Fragment).
GN Name=CD2;
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15302161;
RA Damschroder M.M., Kozhich A.A., Woods R.M., Cheng L., Mullikin B.A.,
RA Wilson S.D., Ulbrandt N.D., Bachy C.M., Wu H., Suzich J.A.,
RA Kiener P.A., Dall'Acqua W.F., White W.I.;
RT "Analysis of human and primate CD2 molecules by protein sequence and
RT epitope mapping with anti-human CD2 antibodies.";
RL Mol. Immunol. 41:985-1000(2004).
DR EMBL; AY445041; AARI5888.1; -.
DR HSP; P08921; IAG4.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0007155; P: cell adhesion; IEA.
DR InterPro; IPR008424; CD2.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF05790; C2-set; 1.
FT NON TER 334
SQ SEQUENCE 334 AA; 37781 MW; EB5F8378B09D80F CRC64;

Query Match 10.0%; Score 212.5; DB 2; Length 334;
Best Local Similarity 24.0%; Pred. No. 0.00014;
Matches 83; Conservative 56; Mismatches 140; Indels 67; Gaps 14;

Qy 45 GTVGKSALLSVQYSSTSSDRPVVKWQKRDKPVTVQSIGTEVIGTLRP-----DYRDR 99
Db 25 GALTQDIDLDIPFQMSDDIDDKWETSCK-----KKIAQFRKEKETEERKDAY 74
Qy 100 RLFPENGSLLSLDLQADGTYVEISITDDTFTEKTNITVDVPIRSPQVLVASTVLE 159
Db 75 KLFKNGTLKIKHLKHQDQSKYSIYDTKGNVLEKTFDLKIQRVSEPKI---SWTCIN 131
Qy 160 LSEFTLNCSHENGTKPSYTLWKDGPLLNDRLSPDQKVL---ITRVLMDDDLYS 216
Db 132 T---TLTCEVMNGTDPFLNLYQDGK-----HVKLS--QRVITHKWTISAK----FK 175
Qy 217 CMVENPISQGRSLPVKITVYRRSSLYIILS-TGGIFLLVTLTVTCACWKPSKRKQKLEK 275
Db 176 CTAGNKVSKESSEVPVSCPEKGLDIYLIIGICGGSLMVVFALLVYITKRKQKS--- 232
Qy 276 QNSLEYMDQNDRLKPEADTLPRSGQERKNPMALYILKDKSPETEENPAPPSATE- 334
Db 233 -----RRNDELEIRAH---RVATEERGRKHQIPASTPONPAASQHPPPPGRHQ 282
Qy 335 -----PGPPGYSVS-----PAVPG-----RSPGLPIRSARYPRSP 365
Db 283 PSRPLPPGHRVQHQPQRPPAPSGTQVHQKGGPLPRPRVQPKPP 328

RESULT 13
Q6SZ57
ID Q6SZ57 PRELIMINARY; PRT; 341 AA.
AC Q6SZ57;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Cluster of differentiation 2 (Fragment).
GN Name=CD2;
OS Macaca arctoides (Stump-tailed macaque).

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